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(54) **Title:** UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

(57) **Abstract:** The invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin and a method for identification of the specific animal from a given biological sample.

UNIVERSAL PRIMERS FOR WILDLIFE IDENTIFICATION

TECHNICAL FIELD

The invention relates to the identification of novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin at species and sub-species sources. The invention also provides a method for the identification of fragments on mitochondrial cytochrome b gene in biological material of unknown origin.

BACKGROUND ART

A large number of studies in evolutionary biology utilize phylogenetic information obtained from mitochondrial cytochrome b gene. It has been identified a potent molecule to distinguish the phylogenetic depth of different lineages to family, genus and species in molecular taxonomy[1-66]. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in public databases such as GenBank, NCBI (http://www.ncbi.nlm.nih.gov) etc. We have utilized this capacity of cytochrome b gene in establishing the identity of the origin of animal parts and product to its family, genus and species sources. The technique developed is based on a pair of universal primer that can amplify a small fragment of cytochrome b gene from a vast range of animal species.

Establishing identity of confiscated animal parts and products is a great challenge to law enforcement agencies because none of the methods available till date is too efficient to reveal the identity of animal remains beyond a reasonable doubt. Morphological markers, described for certain species allow the identification of complete specimen of animals[67]. However, a complete specimen is confiscated very rarely by the investigation agencies; therefore, these marker are not practical in wildlife forensics. The biochemical traits such as the bile characteristics[68] blood heam analysis[69,70] etc. have also been employed in wildlife forensic for identification of individual species. The difficulty of these markers are that these markers are limited in number and are rarely found in their natural forms in which these were originally described as the characteristic of a particular species.

The molecular approaches such as micro-satellite based identification[71], Restriction fragment length polymorphism analysis of mitochondrial genes or PCR based species specific STS markers require the prior information of the species to establish the identity[72,73]. These methods also need a significant amount of DNA material to be analysed. We may not have the prior information about the species origin of confiscated animal parts and product in forensics, therefore, these methods are not really useful and

practical in wildlife identification. The technique invented by us is universal, therefore does not require any background information to establish the identity of any unknown confiscated remains at family, genus and species sources. Being a PCR based procedure it can be applied with trace amount of any biological material. Because the amplicon length is small (472 bp); therefore, it can work perfectly with the mutilated remains, which are commonly seized by the crime investigation agencies. It does not require the large amount of genetic material i.e. DNA to be analyzed to establish the identity, hence, can detect a minute amount of adulteration in food products. The procedure described is simple and very fast. Due to the said advantages, the procedure invented by us is most suited for forensic wildlife identification.

OBJECTS OF THE INVENTION

The main object of the invention is to identify a fragment on mitochondrial cytochrome b gene capable of significantly discriminating among various evolutionary lineages of different animal species.

Another object is to identify a fragment on mitochondrial cytochrome b gene which is flanked by the highly conserved sequences at a vast range of animal species.

Yet another object is to detect a fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.

Still another object is to develop the universal primers to amplify the fragment on mitochondrial cytochrome b gene using polymerase chain reaction.

Another object is to develop a PCR protocol that works universally with DNA template of any unknown origin (i.e. all the animal species).

Yet another object is to provide a universal method for identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

Still another object is to provide a universal method of animal identification to establish the crime with the criminal beyond a reasonably doubt.

Another object is provide a universal method to establish the identity of biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

Yet another object is to provide a universal method for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation to the wildlife resources could be controlled.

Still another object is to provide a universal technique to have an idea of the geographical location of the commitment of wildlife crime based on the haplotype of poached animal identified by the universal primer invented.

Another object is to provide a universal technique of animal identification to detect the adulteration of animal meat/products in vegetarian food product for the purpose of food fortification, by the food fortification agencies.

Yet another object is to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.

Another object is to invent and authenticate a universal technique that can be converted to a (a) <u>'MOLECUALR KIT'</u> and (b) <u>'DNA CHIPS'</u> based application to meet the requirements of above objectives.

SUMMARY OF THE INVENTION

Accordingly, the invention provides novel universal primers that can amplify the fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and reveal the identity of the biological material of any unknown animal origin

DETAILED DESCRIPTION OF THE INVENTION

Keeping in view the above objectives, the cytochrome b gene sequences (1140 bp) of 221 distantly related animal species (listed in Table 1) representing various families were obtained from public database NCBI (<u>http://www.ncbi.nlm.nih.gov</u>). These sequences were aligned using the software *Clustal X(1.8)*(NCBI, USA) and a fragment (of 472 bp, alignment shown in Table 2) of gene was identified which had all the features mentioned above under column 1, 2 and 3 of sub-heading 'Objectives of invention'. As for the *identity of this fragment* we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra:*

"taccatgaggacaaatatctttttgaggagcaacagtcatcaccaatctcctttcagcaatcccatacatcggtacaaacctagtaga atgaatctgaggagggttctcagtagataaagcaacccttacccgatttttcgccttccactttatcctcccatttatcattgcagccctt accatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaattccattccac ccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgcttctagtcctattctcaccggacctgcttggag acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttcctatttgcatacgcaatcct ccgatcaattcctaacaaactaggagg".

A pair of universal primer was designed to amplify this fragment in polymerase chain reaction (PCR). These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of <u>m</u>itochondrial <u>c</u>ytochrome <u>b</u> gene between nucleotides <u>398</u> to <u>869</u> of *Antilope cervicapra,* a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India. These primers work universally because its 3' end are highly conserved amongst a vast range of animal species (shown in Table 2). As mentioned above, the DNA fragment (sequence of which is shown above) targeted by these primers is highly polymorphic inter-specifically; however, it is monomorphic among the individual of same species (Tables 6, 7a, 7b, 7c, 7d and 8, respectively). These unique features of the targeted region enable these primers to generate the molecular signatures of an individual species; thereby, enabling them to differentiate amongst the animals of different species (see in Figure 1c). The variation within the fragment amplified by these primers increase with increasing distances of evolutionary lineages of two animals (Table 8). These unique features of the fragment amplified by the universal primers 'mcb398' and 'mcb869' invented by the applicants fulfill the objectives of invention.

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using '*BLAST* software[73], it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. The complete procedure involved in the *analyses* (the word, '*analyses*' should be understood with the stepwise procedure to establish the identity of the biological remain of any unknown animal origin for the aims mentioned in columns

1-13 under sub-heading 'Objectives of invention') is briefed under 'Examples 5 and 6, respectively, as well as illustrated in Figures 1a, 1b and 1c, respectively.

BRIEF DESCRIPTION OF DRAWING AND TABLES

Figure 1a. Illustration of the step-wise procedure involved in *analyses*. The unknown biological material i.e. 'adil.flesh' refers to the confiscated skin mentioned in 'Example 6'. The arrow marks indicate the stepwise procedure involved. The brief description of Figure 1a is as follows:

The biological material i.e. the confiscated skin 'adil.flesh' was subjected to DNA isolation using the standard procedures[74]. The DNA obtained was amplified using the primers 'mcb398' and 'mcb869' in PCR, fractionated in 2% (w/v) agarose gel, visualized and photographed under UV light using Gel Documentation System (Syngene, USA). The lane 'M' shown in the photograph represents the molecular weight marker (Marker XIII, Boehringer mannheim). Lane 1 shows the PCR amplicon (472 bp) obtained from 'adil.flesh' using primers 'mcb398' and 'mcb869'. The PCR amplicon obtained were sequenced at both the strand using "ABI Prism 3700 DNA Analyzes, PE-Applied Bio-systems). The chromatogram shows the sequences (about 80 bp long, i.e. between 150-230 bp of sequence (328 bp), revealed from the PCR product of 472 bp length) obtained from 'adil.flesh'.

Figure 1b. Illustrates the further steps involved in *analyses*. The sequence (328 bp) revealed from 'adil.flesh' was subjected to homology search in *nr (i.e. non-redundant)* database of Netional Centre for Biological Information (NCBI), USA. The sequences producing significant alignments are shown along with its bits score and E values. It indicates the extent of homology amongst the sequence enquired (i.e. the 328 bp sequence from adil.flesh) and the sequences registered in *nr* database of NCBI. BLAST analysis revealed the highest homology of the sequence revealed from 'adil.flesh' with the sequence of *Panthera pardus* (gene bank registration number 'AY005809'), indicating the identity of adil.flesh as that of a leopard (*Panthera pardus*) origin. Figure 1b further illustrates the multiple alignments of the sequences obtained from reference animals (listed in Table 5) along with the sequence obtained from 'adil.flesh'. The sequences of 'adil.flesh' is similar to the sequences of 'gz1L' further confirming the identity of the source of confiscated remain 'adil.flesh' as that of a *Panthera pardus* origin.

Figure 1c illustrates the NJ-tree (Neighbor Joining tree) constructed using CLUSTAL X (1.8) from the sequences revealed from 'adil.flesh' and reference animals listed in Table 5.

The animals belonging to similar species cluster together; however, the animals of different species group in different clusters. The confiscated material under investigation (i.e. 'adil.flesh') clusters with 'gz1L' (i.e. the known normal leopard *'Panthera pardus'*) indicating the identity of the species of 'adil.flesh' as that of a *Panthera pardus* source.

Figure 2 shows the Agarose gel electrophorogram showing the PCR amplicons (472 bp) obtained from the reference animals of family felidae listed in Table 5, using universal primers 'mcb398 and 'mcb869'. Description of different lanes is as follows:

Lanes 1-21: The PCR profiles of the animals 1-21, respectively, listed in Table 5.

Lane 22: The PCR profiles of DNA isolated from confiscated skin of unknown animal origin 'i.e. adil.flesh'

Lane 23: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

Figure 3. Shows PCR amplicons obtained from animals listed in Table 9. The primers used in PCR are 'AFF' and 'AFR'. The description of different lanes shown is as follows:

Lane 1-4: The PCR profiles of animals 1-4, respectively, listed in Table 9, showing amplicons of 354 bp.

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

Figure 4. Shows PCR amplicons obtained from animals listed in Table 12. This experiment demonstrates the universal nature of our primers among a vast range of animal species. Description of different lanes shown is as follows:

Lanes 1-23: The PCR profiles of the animals 1-23, respectively, listed in Table 12. The PCR product of 472 bp is amplified universally from all the animal species analyzed.

Lane 24: Negative control (no DNA)

Lane M: Molecular weight marker (marker XIII, Boehringer mannheim)

Table 1. List of 221 animal species used for *In-silico* analysis to design the universal *primers 'mcb398' and 'mcb869'. Table also demonstrate the* 'P,S *scores*' of 'mcb398' and 'mcb869' for different templates. The descriptions of various symbols used in this table are as follows:

Symbol (#) refers to Number

Symbol (*) refers to the animal species which is either protected species (listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972), or an endangered/rare animal species

Symbol ($P,S/F) refers to Probability of match and Stability of match of primer 'mcb398' with different templates (i.e. the cytochrome b gene from different species origin). A higher P, S score refers to the higher probabilities of significant amplification of specific

template by the primer. It is calculated by *Amplify (1.2)* software.

Symbol ($^{\Psi}$P,S/R) refers to Probability of match and Stability of match of primer 'mcb869' with different templates. A higher P,S score refers to the higher probabilities of significant amplification of specific template by the primer. It is calculated by *Amplify (1.2)* software.

Table 2. Multiple sequence alignment of 472 bp fragment of mitochondrial cytochrome b gene (identified by inventors to fulfill the requirements of column 1, 2 and 3 mention under sub-heading 'Objectives of invention') of 221 animal species listed in Table 1. Alignments also show the binding sites for universal primers 'mcb398' and 'mcb869'. The symbol (*) refers to the nucleotide bases which are conserved amongst 221 animal species listed in Table 1). The alignments have been done using software *CLUSTAL X (1.8)*. The nucleitide positions that are unmarked are variable amongst 221 animal species analyzed. These variable sites together constitute the molecular signature of an individual species, giving rise to molecular basis of species identification by our primers.

Table 3. Results of the blast analysis of the sequence revealed from 'adil.flesh' in '*mito*' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *felis catus* cytochrome b gene sequence (genbank registration number NC_001700.1, bits score 365, E value, e-101) registered in NCBI database (bits score 365 and E value e-101). It gives an indication that the species of analyzed material belongs to family felidae. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

Table 4. Results of the blast analysis of the sequence revealed from 'adil.flesh' in '*nr*' database of NCBI. It shows the most significant alignment of cytochrome b sequence (328 bp) revealed from confiscated skin piece 'adil.flesh' with *Panthera pardus* cytochrome b gene sequence (genbank registration number AY005809, bits score 603, E value, e-170) registered in NCBI database. It gives an indication that the species of analyzed material belongs to *Panthera paurdus* origin. It also fulfills the requirements of column 6 mention above under sub-heading 'Objectives of invention'.

Table 5. Reference animal belonging to family felidae selected for comparison with 'adil.flesh' to confirm the findings of BLAST analysis results of which are mentioned in Table 3 and 4, respectively. The animals listed in SN. 1-21 represent different species of family felidae. SN. 22 and 23 are primate species taken for out-group comparisons.

Table 6 Multiple sequence alignments of cytochrome b sequences (328 bp) revealed from 'adil.flesh' and reference animals listed in Table 5. The positions that have a common nucleotide in all the animal species under investigation are shown with a star (*) mark;

however, the positions that are variable in any of the animals under investigation are unmarked. The nucleotides at these positions constitute the molecular signature of an individual species, which are unique and highly specific for its species. These signatures are the molecular basis of identification of individual animal species using our primers 'mcb398' and 'mcb869'.

Table 7 (Tables 7a, 7b, 7c and 7d). The comparison of the molecular signatures of different animal species investigated along with 'adil.flesh', the confiscated skin of unknown animal origin. This table demonstrates the variable positions (i.e. the positions which are not marked with star (*) symbol in Table 6), amongst the 328 bp fragment revealed from the animals listed in Table 5. The dot (.) mark represents the presence of the similar nucleotide as listed in lane 1 i.e. the sequence from "adil.flesh' at that position. It demonstrates that the signatures of each species are unique and specific to its species. The molecular signatures of 'adil.flesh' are comparable (except for position 37 which has a transition from 'T' to 'C') to the molecular signature of 'gz1L' i.e. the known leopard *'Panthera pardus'* source, indicating the identity of the source of confiscated skin 'adil.flesh' as that of a leopard *'Panthera pardus'* source. The nucleotide variations (at the positions 153, 198, 223, 264, among the known leopards, (i.e. gz1L, gz2L, and gz3L, respectively)), give an idea about the geographical habitat of each animals. Various studies referring to molecular evolution of different animal species support this hypothesis[75]; however, it could further be confirmed by taking the reference animals from different geographical areas and analyzing by our primers 'mcb 398' and 'mcb869'. If we could generate the database of different haplotypes (i.e. habitat specific molecular signatures) of the animal species, it would also enable our primers to reveal the geographical location of the commitment of wildlife crime.

Table 8. Percent similarity matrix calculated by pair-vise comparisons of nucleotide sequences aligned (illustrated in Table 6). The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity (99.7% and 98.2%, with the lineages of animals 'gz2L' and 'gz3L', respectively) with the sequences obtained from known normal leopard source, indicating its identity as that of a leopard origin. The similarity matrix has been calculated using the software *PHYLIP (3.5)*.

Table 9. Animals selected for validation of minimum P,S score for efficient amplification of cytochrome b gene of different origin by the primers 'mcb398' and 'mcb869'. P,S score of primers 'AFF' and 'AFR' for these animals are shown.

Table 10. BLAST analysis of primers 'mcb398' in *nr* database of NCBI . It demonstrates

that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer

Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

Table 12. Other animal belonging to distantly related animal species, investigated to confirm the universal nature of primers 'mcb398' and 'mcb869'. Gel photograph showing the PCR amplicons from these animals are shown in Figure 4.

The mitochondrial cytochrome b gene has very widely been used in molecular taxonomic studies. It has immense capabilities to reveal different evolutionary lineages of animals in family, genus and species specific manner. It has also been used to classify the population of a particular species according to its demographic distributions[75]. The vast database of cytochrome b sequences of different animal species has accumulated in public databases such as Genbank and NCBI[1-65]. We have explored these unique characteristics of cytochrome b gene to establish the identity of confiscated remains of any unknown animal by inventing a pair of novel primers, 'mcb398' and 'mcb869', that can amplify a small fragment (472 bp) of cytochrome b gene of wide range of animal species in universal manner. These primers work universally because its 3' ends target within a highly conserved region.

The fragment of cytochrome b gene identified had all the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention'. We identified this fragment by aligning the cytochrome b gene sequences (1140 bp) of 221 different animal species listed *in Table 1. These sequences are publicly available in NCBI DNA databases.* These sequences were aligned using the software *CLUSTAL X (1.8).* As mentioned before, the 472 bp fragment of cytochrome b gene identified by us to have the features mentioned in columns 1, 2 and 3 listed under sub-heading 'Objective of invention' includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions (marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, revealing the identity of the biological material belonging to that of an unknown animal origin by the procedure invented by us. As for identity of this fragment we are

considering *Antilope cervicapra* as a representative species, and the sequence the above fragment of cytochrome b gene of *Antilope cervicapra* is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

"taccatgaggacaaatatctttttgaggagcaacagtcatcaccaatctcctttcagcaatcccatacatcggtacaaacctagtaga atgaatctgaggagggttctcagtagataaagcaacccttacccgatttttcgccttccactttatcctcccatttatcattgcagcccctt accatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaaa[illegible]cattccac ccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgcttctagtcctattctcaccggacctgcttggag acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttcctatttgcatacgcaatcct ccgatcaattcctaacaaactaggagg

Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species. Each species in table 2 has been represented by a unique code, which is decoded in Table 1. We selected these species to represent the vast range of animal families of distant orders. Of 221 species, about 65 were the protected/endangered or rare species listed in Wildlife (Protection) Act , 1972 (Central Act NO 53 of 1972). These species are marked with symbol (*) in Table 1. The NCBI accession number refers to its registration number in NCBI database and the number in superscript represent the reference cited. Based on the aligned cytochrome b sequences of different 221 animal species the primers designed were as follow:

Primers name	Sequence (5'-3')
'mcb398'	"TACCATGAGGACAAATATCATTCTG"
'mcb869'	"CCTCCTAGTTTGTTAGGGATTGATCG"

Tables 2, 10 and 11, respectively, demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico* (In total 221 animal species listed in Table 1 and about 500 species listed in Tables 10 and 11, respectively) Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to *improve the probability and stability of match of the primers to their target sequences* (*i.e.* the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., 'Amplify (1.2)', 'Primer3' (http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi) as well as manually. . We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify (1.2)*. The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98.63 (i.e. the situation where the primer has perfect match with template);

however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were *Eumeces egregious* and *Equus ainus*. *Eumeces egregious* had P, S score 86, 55 and 73,51 for 'mcb398' and 'mcb869', respectively; however, the P, S score of *Equus ainus was calculated as* 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'tagtagaatgaatctgaggagg3' and AFR=5'atgcaaataggaagtatcattc3'.) having more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa* These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregious*) for our primers 'mcb398' and 'mcb869', respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregious* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in *a universal manner.*

For further confirmation of universal nature of our primers, we blasted the sequence of our primers against the *mito* and *nr* databases of NCBI using BLAST software. The results of these analyses are shown in Tables 10, and 11, respectively.

Finally, the universal nature of the primers was tested in our laboratory with some more animal species listed in Table 12. These primers amplified all the animal species efficiently, giving rise to the band of expected size (472 bp). The results are shown in Figure 4. This experiments substantiated the results of P,S analysis and other *in-silico* analyses to show that the primers 'mcb398'and 'mcb 869' are universal primers.

The flow chart of establishing identity of the species of biological material of unknown animal origin using primers 'mcb398' and 'mcb869'

Biological material of unknown animal origin

↓

DNA isolation

↓

PCR amplification of DNA isolated using primers 'mcb398' and 'mcb869'

↓

Sequencing at both the strands in triplicate (using any standard procedure of sequencing such as using ABI Prism 3700, PE-Applied Bio-systems)

↓

BLAST of revealed sequence in *mito* database of NCBI (http://www.ncbi.nlm.nih.gov/BLAST (it gives idea about the family of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

↓

BLAST of revealed sequence in *nr* database of NCBI (http://www.ncbi.nlm.nih.gov/BLAST (it gives idea about the Genus or more precisely, species of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

↓

Selection of reference animals belonging to the family/Genus/and species revealed by *mito* and *nr* BLAST searches

↓

Isolation of DNA from the blood of known reference animals; PCR amplification using primers 'mcb398' and 'mcb869' ; sequencing of the PCR products in triplicate using the same primers

↓

Multiple sequence alignments of the revealed sequences of mitochondrial cytochrome b gene of known reference animals and the biological material of unknown animal origin using software such as *Autoassembler (/CLUSTAL X (1.8)*

↓

Identification of sequence from the aligned sequences that is homologous (or significantly similar) to the cytochrome b gene sequence of the DNA obtained from biological material of unknown animal origin.

↓

The species of homologous sequence would be the species of the biological material under investigation

Examples

Example 1

Example for identification of a fragment of cytochrome b gene fulfilling the requirements of columns 1, 2 and 3 mentioned under sub-heading 'Objectives of invention' of heading 'Brief summary of invention'

The cytochrome b molecule has very vastly been used in molecular taxonomic studies. Being a slow evolving gene, It has a tremendous information in its nucleotide sequences to distinguish the animals to their family, genus and species sources[1-65]. A vast database of the sequences of cytochrome b gene of different animal species has accumulated in the *nr* and *mito* databases of NCBI. We have explored these qualities of cytochrome b gene to establish the identity of confiscated remains of unknown animal origin to its family, genus and species sources. For this purpose, we have identified a fragment of cytochrome b gene which is highly polymorphic inter-specifically, however, it is monomorphic among the individual of same species, therefore it can group the individual of an unknown species with the known individuals of reference species to which it belongs. In order to amplify this fragment from DNA isolated form any unknown origin, it was necessary that it remain flanked with the highly conserved sequences amongst a vast range of animal families. To identify such a unique fragment within the cytochrome b gene, we aligned the sequences of 221 distantly related animal species (listed in Table 1) representing various families using software CLUSTAL X (1.8). These sequences were obtained from public database NCBI (http://www.ncbi.nlm.nih.gov). The aligned data was examined carefully for the conserved sites amongst all the species included in *in-silico* analysis. We identified a fragment (472 bp) of cytochrome b gene that was fulfilling all the requirements mentioned above and also under column 1, 2 and 3 of sub-heading 'Objectives of invention'.

As for the identity of this fragment we would like to mention that it includes the nucleotides between 398 to 869 in *Antilope cervicapra* and *Felis catus*; however, 399 to 870 in *Homo sapiens sapiens* species. Except at few positions marked as star (*) in Table 2, the nucleotide sequences of this fragment are highly variable amongst the animal species, giving rise to their unique molecular signature. These molecular signatures are characteristic of its species and form the basis of revealing the identity of the biological material of an unknown animal origin by the procedure invented by us. Considering *Antilope cervicapra* as a representative species, the sequence of this fragment is mentioned herewith:

Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra*

“taccatgaggacaaatatctttttgaggagcaacagtcatcaccaatctcctttcagcaatcccatacatcggtacaaacctagtaga
atgaatctgaggagggttctcagtagataaagcaacccttacccgatttttcgccttccactttatcctcccatttatcattgcagccctt
accatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaaattccattccac
ccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgcttctagtcctattctcaccggacctgcttggag
acccagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttcctatttgcatacgcaatcct
ccgatcaattcctaacaaactaggagg”

Example 2:

Example for development of universal primers to amplify the fragment identified mentioned under ‘Example 1’.

A pair of universal primer was designed which has the following features:

1. It targets the fragment identified (mentioned under ‘Example 1’) to amplify it in polymerase chain reaction (PCR).
2. Its 3’ and 5’ ends that are highly conserved (marked as star (*) in Table 2), amongst a vast range of animal species ensuring the amplification of the fragment mentioned above in a universal manner. The sequencing of the fragment amplified by these primes reveals the molecular signature of the species of analyzed material, which on comparison with the sequences of the known reference animals reveals the identity of the species of unknown biological material under investigation.
3. The tm (melting temperature) of both primers was almost similar (about 58 degree centigrade) ensuring the significant annealing of both the primers to its template, therefore significant amplification of targeted region in PCR.
4. The internal stability and P, S, score of the primers were ensured higher while designing it. The possibilities of internal loop formation, dimmer formation etc were also excluded by selecting its sequence uniquely. This ensured that the primer would be a good primer to be used in PCR for amplification of DNA from unknown animal origin.
5. The 3’ end of the primers were ensured to have either ‘G’ or ‘C’ to increase the probability of strong bonding at its 3’ends, which is necessary for efficient amplification of DNA template in PCR. It also strengthens the universal nature of the primer.
6. The sequences of the primers were ensured to be unique so that it does not give rise to non-specific and spurious products in PCR leading to confusion. It improved the efficiency and quality of the technique invented by us.

7. These primers were named as 'mcb398' and 'mcb869' because of its property to amplify a region of mitochondrial cytochrome b gene between nucleotides 398 to 869 of *Antilope cervicapra*, a representative animal species for this invention. We took this animal species as representative species because the idea of developing such a novel primers came in the mind of inventors while they were working on the genome of this animal in Centre for Cellular and Molecular Biology, Hyderabad, India.
8. The sequences of the universal primers invented are as follows:

Primers name	Sequence (5'-3')
'mcb398'	"TACCATGAGGACAAATATCATTCTG"
'mcb869'	"CCTCCTAGTTTGTTAGGGATTGATCG"

Example 3:

Example for development of universal PCR conditions to ensure the amplification of a template of any unknown origin in PCR, hence strengthening the universal nature of the technique invented by us

The PCR conditions developed had the following unique features:

1 These were capable of amplifying the DNA template of any animal origin in an universal manner using the universal primers mentioned under 'Example 2'.

2. The conditions were selected to ensure the comparable annealing temperature for both the primers i.e. 'mcb398' and 'mcb869'.

3. The PCR conditions standardized herewith are universal; therefore, the possibility of PCR failure with a template of unknown origin due to non-standard conditions is excluded. It ensures the universal nature of our technique to be used in wildlife forensics.

4. *The universal conditions mentioned above are:*

Amplification reactions should be carried out in 20 μl reaction volume containing approximately 20 ηg of template DNA, 100μm each of dNTPs, 1.25 pmole of each primer, 1.5mM $MgCl_2$, 0.5 unit of Ampli*Taq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95^0C for 10 min, followed by 35 cycles each of denaturation at 95^0C for 45 s, annealing at 51^0C for 1 min, and extension at 72^0C for 2 min. The extension step at 35^{th} cycles should be held for 10 min.

Example 4:

Establishing the universal nature of our primer and experimental evidences to demonstrate the universal nature of primers:

The universal nature of the primers 'mcb398' and 'mcb 869' was ensured by the following measures:

(a) Selecting the primers from the aligned cytochrome b gene sequences of 221 animal of distantly related species:

The cytochrome b gene sequences (1140 bp) were aligned using software *CLUSTAL X (1.8)*. The region of cytochrome b gene that was most conserved amongst 221 animal species was selected to design the primers.

(b) Selecting the 3' and 5' ends of the primers at the highly conserved positions of cytochrome b gene:

The 3' and 5' ends of the primers were ensured to anneal to a highly conserved position amongst 221 animal species representing a vast range of animal families. It was done to ensure an efficient amplification of all the species in PCR. These positions are shown with star (*) mark in Table 2.

(c) Ensuring either 'G' or 'C' at the 3' end of the primers:

It was ensured the primers to have either 'G' or 'C' at its 3' ends as these are the nucleotides that ensure the strong bonding at the 3' ends of the primers due to three hydrogen bonds while pairing with each other. The strong bonding at 3' ends helps the primers to anneal properly with its template resulting in significant amplification in PCR.

(d) Selecting the sequences of the primers to ensure a higher internal stability, higher P, S score, and no primer dimmer and loop formation:

The sequences of the primers were selected to have a high P, S score for a vast range of animal species (Shown in Table 1). The care was taken to exclude the possibilities of loop or primer dimmer formation that could reduce the efficiency of the primers in PCR.

(e) Selecting the sequence of the primers with a comparable melting temperature:

The sequences of the primers were selected to have a comparable melting temperature so that these could work together to amplify a DNA template in PCR at a similar annealing temperature. The melting temperature of both the primers was about 58 degree centigrade and the annealing temperature used in PCR is 51 degree centigrade.

Experimental evidences to demonstrate the universal nature of primers:

(1) Evidence from *In-silico* analysis :

(a) Selecting the primers within the most conserved region of mitochondrial cytochrome b gene

As mentioned above, the primers were designed to anneal within a highly conserved region of mitochondrial cytochrome b gene fragment of 472 bp. Table 2 presents the alignment of the above fragment of cytochrome b gene of 221 animal species representing a vast range of animal families. The conserved positions of nucleotide sequences are shown with star (*) mark in Table 2

Table 2 also demonstrates that the 3' ends of the primers are highly conserved amongst all the animal species analyzed *in-silico.* In the aligned sequences, the conserved nucleotides are marked with symbol (*). Also, the 5' end of the primers were selected within the conserved region of cytochrome b gene to improve the probability and stability of match of the primers to their target sequences (i.e. the above mentioned 472 bp fragment of cytochrome b gene). The primers were thoroughly checked for internal stabilities, loop or dimmer formation using different software viz., *'Amplify (1.2)', 'Primer3'* (http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi) as well as manually.

(b) P, S, score analysis:

We assigned the P,S score (P=Probability of match, S=Stability of match) to the primers for each template using the software *Amplify (1.2).* The higher scores of P and S ensure a good amplification if all other conditions standard (which are mentioned under 'Example 3') are optimum. The Highest score for 'mcb398' was 98,63 (i.e. the situation where the primer has perfect match with template); however, the highest P, S for 'mcb869' was recorded as 98, 68 for a complete match between the primer and template. The lowest P,S score observed for 'mcb398' was 81,50 for species *Talpa europaea* whereas 'mcb869' had a high P, S score for this species (92, 57). The another species which have lowest P, S score for one of the two primers were *Eumeces egregious* and *Equus ainus. Eumeces egregious* had P, S *score 86, 55 and 73,51 for* 'mcb398' *and* 'mcb869', respectively; however, the P, S score of *Equus ainus was calculated as* 91,61 and 73, 51 for 'mcb398' and 'mcb869', respectively. All other animals had higher P, S scores then the above mentioned species. To ensure that these primers would work efficiently with the DNA template from the animals having the lowest P, S score for one of the primers, we designed an another experiment to validate the lower limits of one of the two primers sufficient for efficient amplification in PCR. We designed an another primer pair (AFF= 5'ctagtagaatgaatctgaggagg3' and AFR= 5'tatgcaaataggaagtatcattc3'.) that have more mis-pairing at their annealing sites (but not at ends), therefore have less internal stability

and lower P, S scores for its templates (listed in Table 9). The P,S scores of 'AFF' and 'AFR' were as calculated as low as 41 and 49 for *Platanista gangetica* and *Sus scrofa* These species were amplified efficiently using the primers 'AFF' and 'AFR' (results shown in Figure 3) (keeping all other conditions standard i.e. the conditions mentioned in 'Example 3'). The lowest P,S scores (86, 55 and 73,51 for species *Eumeces egregious*) for our primers 'mcb398' and 'mcb869', respectively, were higher then the above range of combined P, S scores of 'AFF' and 'AFR' for species *Sus scrofa* (87, 52 and 87, 41), which was efficiently amplified by the primers 'AFF' and 'AFR'. It gives an indication that the primers 'mcb 398' and 'mcb 869' would work with all the species including *Eumeces egregious* efficiently to give rise to the expected product in PCR. This experiment confirmed that the primers 'mcb398' and 'mcb 869' are capable of amplifying the cytochrome b fragment of most of the animal species in a universal manner.

© BLAST analysis:

The sequences of primers 'mcb398' and 'mcb869' were blasted against mito and nr databases of NCBI to see its significant alignments with the sequences registered in GenBank. As expected, the most significant alignments of the sequences were found with the cytochrome b gene regions (within the 472 bp fragment mentioned in 'Example 1') of different animal species. This analysis also showed that the 3' as well as 5' ends of the primers were highly conserved amongst a vast range of animal species, confirming the universal nature of the primers (Tables 10 and 11, respectively)

(2) Evidence from bench work/experiments done in laboratory conditions:

The DNA from different animals belonging to distantly related species (mentioned in Table 12) was isolated and subjected to PCR amplification using the primers invented by us i.e. the primers 'mcb398' and 'mcb869' The PCR products amplified were resolved in agarose gel by electrophoresis and visualized under UV light. The PCR products of expected size (472bp) were obtained from all the animals confirming the universal nature of our primers. These results are shown in Figure 4.

Example 5:

Example to establish the identity of confiscated remains from unknown animal origin using the universal primers 'mcb398' and 'mcb869'.

The step-vise procedure to establish the identity of the biological material from an unknown animal source is mentioned below:

Biological material of unknown animal origin

DNA isolation

PCR amplification of DNA isolated using primers 'mcb398' and 'mcb869'

Sequencing at both the strands in triplicate (using any standard procedure of sequencing such as using ABI Prism 3700, PE-Applied Bio-systems)

BLAST of revealed sequence in *mito* database of NCBI (http://www.ncbi.nlm.nih.gov/BLAST

(it gives idea about the family of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

BLAST of revealed sequence in *nr* database of NCBI (http://www.ncbi.nlm.nih.gov/BLAST

(it gives idea about the Genus or more precisely, species of the analyzed material by producing the most significant alignment of the query sequence with the sequences registered in database)

Selection of reference animals belonging to the family/Genus/and species revealed by *mito* and *nr* BLAST searches

Isolation of DNA from the blood of known reference animals;

PCR amplification using primers 'mcb398' and 'mcb869' ; sequencing of the PCR products in triplicate using the same primers

Multiple sequence alignments of the revealed sequences of mitochondrial cytochrome b gene of known reference animals and the biological material of unknown animal origin using software such as *Autoassembler/CLUSTAL X (1.8)*

↓

Identification of sequence from the aligned sequences that is homologous (or significantly similar) to the cytochrome b gene sequence of the DNA obtained from biological material of unknown animal origin.

↓

The species of homologous sequence would be the species of the biological material under investigation

↓

Application of the above information for the objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

Example 6:

The actual execution of the technique invented

As a first application and to demonstrate the ease and utility of this method, we investigated a case of forensic identification submitted at our laboratory to seek scientific opinion on animal hunting evidence. In this case, we received the half burned remains of an unknown animal, confiscated by the crime investigation agencies. The DNA was isolated from the above material following standard methods[74] and subjected to PCR amplification using the primers mentioned above (viz., 'mcb398' and 'mcb869'). Amplification reactions were carried out in 20 μl reaction volume containing 20 ηg of template DNA, 100μm each of dNTPs, 1.25 pmole of each primer, 1.5mM $MgCl_2$, 0.5 unit of Ampli*Taq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer *(10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed were: an* initial denaturation at 95^{0}C for 10 min, followed by 35 cycles each of denaturation at 95^{0}C for 45 s, annealing at 51^{0}C for 1 min, and extension at 72^{0}C for 2 min. The extension step at 35th cycles was held for 10 min.

The PCR products obtained were sequenced in automated work station (ABI Prism 3700, PE-Biosystems) on both strands in triplicate and the sequence resolved (328 bp, shown in Figure 1a) was blasted against *mito* databases of NCBI using BLAST program[73]. The most significant alignment (bits Value 365, E value e^{-101}) of this sequence was produced with the cytochrome b gene sequence of *Felis catus*, (Table 3) indicating that species of

analyzed material belongs to family felidae. Further, the above sequence revealed from the confiscated remain was blasted against *nr* databases of NCBI using BLAST program. The most significant alignment (bits Value 603, E value e^{-170}) of this sequence was produced with the cytochrome b gene sequence of *Panthera pardus* (Table 4), indicating the identity of the analyzed material as that of a *Panthera pardus* source. Based on this information, we selected the reference animals listed in Table 5 representing different species and subspecies of felidae. The DNA isolated from reference animals was amplified and sequenced on both strands in triplicate using the primer pair mentioned above. Consensus sequences obtained were aligned using program *CLUSTAL X (1.8)* (Table 6). Sequence comparisons identified 113 variable sites in total amongst all animals analyzed (Table 7). Pair-vise comparisons of sequences were performed to find out the variation among different animals investigated. All the species investigated were differentiated by a their unique nucleotides sequences. The molecular signatures of different reference animals were compared with the molecular signature of the confiscated skin 'adil.flesh'. Table 7 demonstrate that the maximum similarity of the adil.flesh with 'gz1l' i.e. known Leopard (*Panthera pardus*) species, indicating the identity of the adil.flesh, the confiscated skin, as that of a Panthera pardus origin. We also calculated the similarity matrix showing the pair-vise similarity amongst the animal species under investigation using *PHYLIP* software This matrix is shown in Table 8. It demonstrates that the animals belonging to different species had more variation; however, the animals of same species had maximum similarity among their cytochrome b sequences. The cytochrome b gene sequence of DNA isolated from confiscated material had maximum similarity with the sequences obtained from known Leopard source(99.7%, and 98.2 with 'gz1l' and 'gz2l', respectively); establishing the identity of the source of confiscated material as that of a Normal leopard (*Penthera pardus*) species. The step-vise procedure involved in above analysis is illustrated in Figure 1a, *1b and 1c, respectively.*

Thus, the primers invented by us can generate the molecular signature from any biological material of unknown animal origin, which actually is the characteristic of its family, genus and more precisely, the species. When these signatures are compared *in-silico* with the signatures already available in public databases (viz., GenBank, NCBI database etc) using *BLAST* software[73], it indicates identity of the family, genus or species of the analyzed material, which in turn is confirmed practically by comparing with the reference animals of the revealed family, genus or species, by including them in the further analysis by the primers 'mcb398' and 'mcb869'. Application of the information revealed could be in

fulfilling the requirements of objectives mentioned in columns 7-13 under sub-heading 'Objective of invention' of heading 'Summary of invention'

The method of the invention can be used to establish the identity of confiscated animal parts and products is one of the key requirements of wildlife identification in forensics. It is needed to establish the crime with the criminal beyond a reasonable doubt to avoid the human violation of wildlife resources. Various morphological biochemical and molecular approaches have been given for this purpose; however, none of the current methods is universally applicable to detect the mutilated animal remains of unknown origin. We have identified a fragment on the mitochondrial cytochrome b gene, which has enormous information to differentiate among various animal species back to the family, genus and species sources. We have also found that this fragment is flanked by the highly conserved sequences amongst a vast range of animal species. We invented a pair of universal primer that can amplify this fragment of DNA isolated from the biological material of an unknown animal origin in polymerase chain reaction (PCR) to reveal its identity at species and sub-species sources. This novel invention has great potential to revolutionize the whole scenario of wildlife forensic identification and crime investigation.

Table 1. The animal species included in the study for *in-silico* analysis

SN.	Code	Name	NCBI accession #	$P,S/F	*P,S/R
1	aep.mel	*Aepyceros melampus*	AF036289[1]	97, 60	94, 62
2	ore.ore	*Oreotragus oreotragus*	AF036288[1]	88, 52	94, 62
3	add.nas	*Addax nasomaculatus*	AF034722[2]	97, 60	95, 66
4	ory.dam	*Oryx damah*	AJ222685[1]	90, 58	95, 66
5	hip.equ	*Hippotragus equinus*	AF022060[3]	98, 63	85, 55
6	alc.bus	*Alcelaphus buselaphus*	AJ222681[1]	97, 60	98, 68
7	sig.lic	*Sigmoceros lichtensteinii*	AF034967[4]	97, 60	98, 68
8	bea.hun	*Beatragus hunteri*	AF034968[4]	97, 60	94, 62
9	dam.lun	*Damaliscus lunatus*	AF016635[3]	97, 60	77, 55
10	con.tau	*Connochaetes taurinus*	AF016638[3]	82, 56	93, 62
11	bis.bon	*Bison bonasus*	Y15005[5]	90, 58	87, 63
12	bos.gru	*Bos grunniens* *	AF091631[6]	90, 58	94, 62
13	bos.tra	*Bos tragocamelus* *	AJ222679[1]	90, 58	95, 66
14	buba.bub	*Bubalus bubalis* *	D34637[7]	97, 60	93, 64
15	bub.min	*Bubalus mindorensis*	D82895[8]	97, 60	87, 62
16	tra.ang	*Tragelaphus angasii*	AF091633[6]	97, 60	87, 63
17	tra.eur	*Tragelaphus eurycerus*	AF036276[1]	90, 58	97, 64
18	nem.cau	*Nemorhaedus caudatus* *	U17861[9]	95, 61	93, 59
19	pse.nay	*Pseudois nayaur*	AF034732[2]	89, 55	89, 59
20	amm.ler	*Ammotragus lervia*	AF034731[2]	94, 58	97, 63
21	cap.fal	*Capra falconeri* *	D84202[10]	98, 63	95, 66
22	cap.ibe	*Capra ibex* *	AF034735[2]	98, 63	89, 58
23	hem.jem	*Hemitragus jemlahicus* *	AF034733[2]	95, 61	90, 61
24	rup.pyr	*Rupicapra pyrenaica*	AF034726[2]	95, 61	89, 59
25	rup.rup	*Rupicapra rupicapra*	AF034725[2]	95, 61	94, 64
26	pan.hod	*Pantholops hodgsoni*	AF034724[2]	98, 63	95, 66
27	bud.tax.tax	*Budorcas taxicolor taxicolor* *	U17868[9]	90, 58	95, 66
28	ovi.amm	*Ovis ammon* *	AF034727[2]	98, 63	97, 64
29	ovi.vig	*Ovis vignei* *	AF034729[2]	98, 63	97, 64
30	cap.cri	*Capcornis crispus* *	AJ304502[11]	98, 63	94, 63
31	ovi.mos	*Ovibos moschatus*	U17862[9]	98, 63	92, 61
32	ore.ame	*Oreamnos americanus*	AF190632[12]	98, 63	94, 62
33	cep.dor	*Cephalophus dorsalis*	AF091634[6]	97, 58	90, 61
34	cep.max	*Cephalophus maxwellii*	AF096629[13]	97, 60	88, 53
35	alc.alc	*Alces alces*	AJ000026[14]	95, 61	93, 59
36	hyd.ine	*Hydropotes inermis*	AJ000028[14]	97, 60	90, 63
37	mun.mun	*Muntiacus muntjak* *	AF042718[15]	90, 58	93, 64
38	cer.ele.kan	*Cervus elaphus kansuensis* *	AB021098[16]	98, 63	82, 59
39	cer.ele.xan	*Cervus elaphus xanthopygus* *	AB021097[16]	98, 63	82, 59
40	cer.ele.can	*Cervus elaphus canadensis* *	AB021096[16]	98, 63	90, 61
41	cer.nip.ce	*Cervus nippon centralis*	AB021094[16]	98, 63	90, 61
42	cer.nip.ye	*Cervus nippon yesoensis*	AB021095[16]	98, 63	90, 61
43	cer.nip.ke	*Cervus nippon keramae*	AB021091[16]	98, 63	90, 61

44	cer.nip.pu	*Cervus nippon pulchellus*	AB021090[16]	98, 63	90, 61
45	cer.nip.ni	*Cervus nippon nippon*	AB021093[16]	98, 63	90, 61
46	cer.ela.sc	*Cervus elaphus scoticus*	AB021099[16]	98, 63	90, 61
47	cer.dam	*Cervus dama*	AJ000022[14]	98, 63	88, 53
48	ran.tar	*Rangifer tarandus*	AJ000029[14]	98, 63	89, 57
49	mos.fus	*Moschus fuscus* *	AF026888[17]	90, 59	90, 61
50	mos.leu	*Moschus leucogaster* *	AF026889[17]	90, 59	90, 61
51	mos.chr	*Moschus chrysogaster* *	AF026887[17]	90, 59	90, 61
52	mos.ber	*Moschus berezovskii* *	AF026886[17]	90, 59	90, 61
53	mos.mos	*Moschus moschiferus* *	AF026883[17]	90, 59	92, 61
54	kob.ell	*Kobus ellipsiprymnus*	AF022059[3]	91, 61	95, 66
55	kob.meg	*Kobus megaceros*	AJ222686[1]	91, 61	83, 56
56	red.aru	*Redunca arundinum*	AF096628[13]	91, 61	94, 62
57	red.ful	*Redunca fulvorufula*	AF036284[1]	89, 57	94, 62
58	neo.mos	*Neotragus moschatus*	AJ222683[1]	89, 57	94, 62
59	pel.cap	*Pelea capreolus*	AF022055[3]	91, 61	90, 61
60	ant.cer	*Antilope cervicapra* *	AF022058[3]	82, 56	93, 64
61	sai.tat	*Saiga tatarica*	AF064487[18]	91, 61	92, 61
62	gaz.dam	*Gazella dama*	AF025954[3]	91, 61	92, 61
63	our.our	*Ourebia ourebi*	AF036288[1]	82, 56	82, 59
64	gaz.gaz	*Gazela gazella* *	AJ222682[1]	91, 61	89, 57
65	rap.mel	*Raphicerus melanotis*	AF022053[3]	81, 54	80, 50
66	mad.kir	*Madoqua kirkii*	AF022070[3]	90, 58	97, 65
67	ant.ame	*Antilocapra americana*	AF091629[6]	98, 63	98, 68
68	tra.jav	*Tragulus javanicus* *	D32189[19]	86, 57	86, 59
69	tra.nap	*Tragulus napu* *	X56288[20]	81, 52	93, 58
70	bal.acu	*Balaenoptera acutorostrata*	X75753[21]	89, 56	97, 61
71	bal.bon	*Balaenoptera bonaerensis*	X75581[21]	89, 56	93, 59
72	bal.bor	*Balaenoptera borealis* *	X75582[21]	89, 56	93, 59
73	bal.edi	*Balaenoptera edeni*	X75583[21]	89, 56	88, 54
74	esc.rob	*Eschrichtius robustus* *	X75585[21]	97, 61	86, 57
75	bal.mus	*Balaenoptera musculus* *	NC_001601[22]	97, 57	93, 59
76	meg.nov	*Megaptera novaeangliae* *	X75584[21]	97, 61	94, 63
77	bal.phy	*Balaenoptera physalus* *	NC_001321[23]	97, 57	94, 63
78	cap.mar	*Caperea marginata*	X75586[21]	93, 55	91, 53
79	cep.com	*Cephalorhynchus commersonii*	AF084073[24]	85, 51	88, 55
80	cep.eut	*Cephalorhynchus eutropia* *	AF084072[24]	85, 51	92, 59
81	lag.obl	*Lagenorhynchus obliquidens*	AF084067[24]	94, 59	92, 59
82	cep.hea	*Cephalorhynchus heavisidii*	AF084070[24]	89, 56	97, 63
83	cep.hec	*cephalorhynchus hectori* *	AF084071[24]	89, 56	92, 59
84	lag.aus	*Lagenorhynchus australis*	AF084069[24]	86, 54	92, 59
85	lag.cru	*Lagenorhynchus cruciger*	AF084068[24]	86, 54	92, 59
86	lag.obs	*Lagenorhynchus obscurus*	AF084066[24]	86, 54	92, 59
87	lis.bor	*Lissodelphis borealis*	AF084064[24]	85, 51	92, 59
88	lis.per	*Lissodelphis peronii*	AF084065[24]	86, 54	92, 59
89	glo.mac	*Globicephala macrorhynchus*	AF084055[24]	94, 59	88, 55
90	glo.mel	*Globicephala melas*	AF084056[24]	94, 59	88, 55
91	fer.att	*Feresa attenuata* *	AF084052[24]	94, 59	92, 59

92	pep.ele	*Peponocephala electra**	AF084053[24]	94, 59	88, 55
93	gra.gri	*Grampus griseus*	AF084059[24]	97, 61	89, 59
94	pse.cra	*Pseudorca crassidens**	AF084057[24]	94, 59	92, 59
95	lag.acu	*Lagenorhynchus acutus*	AF084075[24]	98, 63	89, 59
96	orci.bre	*Orcinus orca*	AF084061[24]	86, 57	82, 52
97	orca.bre	*Orcaella brevirostris*	AF084063[24]	86, 57	91, 54
98	del.cap	*Delphinus capensis*	AF084087[24]	96, 54	97, 63
99	del.tro	*Delphinus tropicalis*	AF084088[24]	97, 57	97, 63
100	del.del	*Delphinus delphis*	AF084085[24]	97, 57	97, 63
101	sten.cly	*Stenella clymene*	AF084083[24]	97, 57	97, 63
102	sten.coe	*Stenella coeruleoalba*	AF084082[24]	97, 57	97, 66
103	tur.adu	*Tursiops aduncus*	AF084092[24]	97, 57	97, 63
104	sten.fro	*Stenella frontalis*	AF084090[24]	97, 57	97, 63
105	saus.chi	*Sousa chinensis*	AF084080[24]	97, 57	88, 59
106	sten.lon	*Stenella longirostris*	AF084103[24]	97, 61	97, 63
107	turs.tru	*Tursiops truncatus*	AF084095[24]	97, 57	96, 59
108	lage.alb	*Lagenorhynchus alborostris*	AF084074[24]	97, 61	97, 66
109	sten.bre	*Steno bredanensis*	AF084077[24]	97, 61	94, 64
110	sota.flu	*Sotalia fluviatilis*	AF304067[25]	97, 61	97, 63
111	del.leu	*Delphinapterus leucas*	U72037[26]	97, 61	95, 66
112	mono.mon	*Monodon monoceros*	U72038[26]	97, 61	95, 66
113	plat.gan	*Platanista gangetica**	AF304070[25]	97, 61	86, 59
114	plat.min	*Platanista minor**	X92543[27]	97, 61	86, 59
115	kogi.bre	*Kogia breviceps*	U72040[26]	97, 59	90, 63
116	kogi.sim	*Kogia simus*	AF304072[25]	96, 55	92, 63
117	phys.cat	*Physeter catodon*	AF304073[25]	97, 57	80, 58
118	lipo.vex	*Lipotes vexillifer**	AF304071[25]	89, 56	88, 53
119	phoc.sin	*phocoena sinus*	AF084051[24]	87, 49	92, 62
120	bera.bai	*Berardius bairdii*	X92541[27]	96, 55	90, 59
121	ziph.car	*Ziphius cavirostris*	X92540[27]	97, 61	89, 57
122	meso.eur	*Mesoplodon europaeus*	X92537[27]	97, 57	90, 61
123	meso.bid	*Mesoplodon bidens*	X92538[27]	97, 61	92, 61
124	meso.den	*Mesoplodon densirostris*	X92536[27]	91, 61	94, 63
125	hype.amp	*Hyperoodon ampullatus**	X92539[27]	97, 61	90, 65
126	meso.per	*Mesoplodon peruvianus*	AF304074[25]	97, 61	86, 58
127	pont.bla	*Pontoporia blainvillei*	AF304069[25]	92, 59	88, 55
128	hipp.amp	*Hippopotamus amphibius*	Y08813[29]	92, 58	95, 66
129	hex.lib	*Hexaprotodon liberiensis*	Y08814[29]	98, 63	97, 66
130	rhin.son	*Rhinoceros sondaicus**	AJ245725[30]	90, 59	87, 61
131	cera	*Ceratotherium simum*	NC_001808[32]	90, 59	90, 63
132	dic.sum	*Dicerorhinus sumatrensis*	AJ245723[30]	90, 59	86, 57
133	equu	*Equus asinus*	NC_001788[31]	91, 61	73, 51
134	baby.bab	*Babyrousa babyrussa*	Z50106[33]	89, 56	85, 56
135	phac.afr	*Phacochoerus africanus*	Z50090[33]	90, 59	87, 54
136	sus.scr.ew	*Sus scrofa haplotype EWB3**	AF136549[34]	97, 57	83, 54
137	sus.bar	*Sus barbatus*	Z50107[33]	97, 57	85, 55
138	lama.gla	*Lama glama*	U06429[33]	89, 55	85, 53
139	lama.gua	*lama guanicoe*	Y08812[29]	88, 54	86, 57

140	vic.vic	*Vicugna vicugna*	U06430[35]	89, 55	85, 53
141	cam.bac	*Camelus bactrianus*	U06427[35]	94, 58	86, 58
142	arc.for	*Arctocephalus forsteri*	X82293[36]	97, 60	87, 64
143	arc.gaz	*Arctocephalus gazella*	X82292[36]	94, 58	87, 64
144	eum.jub	*Eumetopias jubatus*	X82311[36]	97, 57	86, 57
145	zal.cal	*Zalophus californianus*	X82310[36]	89, 55	86, 57
146	odo.ros	*Odobenus rosmarus*	X82299[36]	91, 61	81, 52
147	pho.vit	*Phoca vitulina*	X82306[36]	90, 58	87, 64
148	pho.fascia	*Phoca fasciata*	X82302[36]	98, 63	95, 66
149	pho.gro	*Phoca groenlandica*	X82303[36]	92, 59	90, 61
150	cys.cri	*Cystophora cristata*	X82294[36]	89, 56	87, 64
151	hyd.lep	*Hydrurga leptonyx*	X82297[36]	89, 55	82, 54
152	lep.wed	*Leptonychotes weddelli*	X72005[37]	98, 63	91, 66
153	mir.leo	*Mirounga leonina*	X82298[36]	89, 55	82, 59
154	eri.bar	*Erignathus barbatus*	X82295[36]	89, 56	87, 63
155	mon.sch	*Monachus schauinslandi*	X72209[37]	91, 61	87, 60
156	hela.mal	*Helarctos malayanus* *	U18899[38]	84, 54	90, 63
157	sel.thi	*Selenarctos thibetanus* *	AB020910[39]	89, 57	87, 64
158	ail.ful	*Ailurus fulgen* *s	X94919[40]	93, 55	87, 64
159	fel	*Felis catus*	NC_001700[41]	85, 56	90, 63
160	can	*Canis familiaris*	NC_002008[42]	98, 58	84, 54
161	tal	*Talpa europaea*	NC_002391[43]	81, 50	92, 57
162	gla.sab	*Glaucomys sabrinus*	AF011738[44]	90, 59	82, 54
163	gla.vol	*Glaucomys volans*	AB030261[45]	90, 59	87, 60
164	hyl.pha	*Hylopetes phayrei* *	AB030259[45]	91, 61	81, 50
165	pet.set	*Petinomys setosus* *	AB030260[45]	91, 61	81, 50
166	bel.pea	*Belomys pearsonii* *	AB030262[45]	91, 61	87, 64
167	pte.mom	*Pteromys momonga* *	AB030263[45]	97, 61	90, 63
168	gala.demi	*Galagoides demidoff*	AF271411[46]	97, 58	87, 64
169	pero.pot	*Perodicticus potto*	AF271413[46]	97, 60	87, 63
170	gala.mat	*Galago matschiei*	AF271409[46]	97, 60	90, 61
171	gala.moh	*Galago moholi*	AF271410[46]	97, 57	95, 66
172	oto.gar	*Otolemur garnettii*	AF271412[46]	92, 58	87, 60
173	lor.tar	*Loris tardigradus* *	U53581[47]	97, 60	93, 59
174	nyc.cou	*Nycticebus coucang* *	U53580[47]	97, 60	95, 66
175	mus	*Mus musculus*	NC_001569[48]	97, 60	86, 59
176	gorr	*Gorilla gorilla*	NC_001645[49]	89, 57	80, 58
177	homo	*Homo sapiens sapiens*	NC_001807[50]	96, 55	84, 64
178	dug.dug	*Dugong dugong* *	U07564[51]	97, 60	89, 59
179	ele.max	*Elephas maximus* *	AB002412[52]	97, 60	76, 57
180	afr.con	*Afropavo congensis*	AF013760[53]	97, 58	87, 63
181	pavo.mut	*Pavo muticus* *	AF013763[53]	97, 57	87, 63
182	tra.bly	*Tragopan blythii* *	AF200722[54]	89, 55	85, 57
183	tra.sat	*Tragopan satyra* *	AF229837[54]	89, 55	86, 61
184	tra.cob	*Tragopan caboti*	AF200723[54]	89, 55	86, 61
185	tra.tem	*Tragopan temminckii* *	AF028802[53]	89, 55	81, 56
186	arg.arg	*Argusianus argus*	AF013761[53]	89, 55	87, 63
187	cat.wal	*Catreus wallichii* *	AF028792[53]	88, 54	85, 57

188	cro.cro	*Crossoptilon crossoptilon* *	AF028794[53]	89, 55	85, 57
189	sym.ree	*Syrmaticus reevesi* *	AF028801[53]	89, 55	85, 57
190	bam.tho	*Bambusicola thoracica* *	AF028790[53]	80, 48	94, 64
191	fra.fra	*Francolinus francolinus*	AF013762[53]	97, 58	86, 61
192	ith.cru	*Ithaginis cruentus* *	AF068193[53]	98, 63	85, 57
193	ant.par	*Anthropoides paradisea*	U27557[56]	85, 56	82, 58
194	ant.vir	*Anthropoides virgo*	U27545[56]	84, 54	82, 52
195	gru.ant.an	*Grus antigone antigone*	U11060[57]	90, 58	87, 63
196	gru.ant.gi	*Grus antigone gillae*	U11064[57]	90, 58	87, 63
197	gru.any.sh	*Grus antigone sharpei*	U11061[57]	90, 58	87, 63
198	gru.leu	*Grus leucogeranus* *	U27549[56]	90, 58	87, 63
199	gru.can.pr	*Grus canadensis pratensis*	U27553[56]	97, 60	87, 63
200	gru.can.ro	*Grus canadensis rowani*	U27552[56]	97, 60	87, 63
201	gru.can.ta	*Grus canadensis tabida*	U27551[56]	98, 63	87, 63
202	gru.can.ca	*Grus canadensis canadensis*	U27554[56]	97, 61	87, 63
203	gru.ame	*Grus americana*	U27555[56]	90, 58	87, 63
204	gru.gru	*Grus grus*	U27546[56]	89, 54	87, 63
205	gru.mon	*Grus monacha* *	U27548[56]	90, 58	87, 63
206	gru.nig	*Grus nigricollis* *	U27547[56]	90, 58	87, 63
207	gru.jap	*Grus japonensis*	U27550[56]	81, 54	87, 63
208	cic.boy	*Ciconia boyciana* *	NC_002196[58]	94, 58	79, 60
209	rhe.ame	*Rhea americana*	AF090339[59]	93, 63	79, 60
210	ant.alb	*Anthracoceros albirostris* *	U89190[60]	97, 61	86, 59
211	fal.fam	*Falco femoralis*	U83310[61]	97, 61	86, 60
212	fal.ver	*Falco verpertinus*	U83311[61]	97, 61	85, 57
213	fal.par	*Falco peregrinus* *	U83307[61]	97, 61	84, 52
214	fal.spa	*Falco sparverius*	U83306[61]	92, 59	80, 51
215	ayt.ame	*Aythya americana*	NC_000877[62]	98, 63	94, 62
216	smi.sha	*Smithornis sharpei*	NC_000879[59]	97, 58	90, 61
217	vid.cha	*Vidua chalybeata*	NC_000880[59]	97, 60	87, 64
218	chry.pic	*Chrysemys picta*	NC_002073[63]	89, 56	86, 57
219	emy.orb.ku	*Emys orbicularis*	AJ131425[64]	90, 59	94, 63
220	che.mud	*Chelonia mydas* *	AB012104[65]	90, 58	94, 63
221	eum.egr	*Eumeces egregius*	AB016606[65]	86, 55	73, 51

Table 2. Multiple sequence alignment of 472 bp fregment of mitochondrial cytochrome b gene of 221 animal species

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PRIMER 'mcb398'   TACCATGAGGACAAATATCATTCTG
                  * ** ** ** ** ** ** ** ** ** *  *  ** ** ** ** ** *    ** **
                  TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACAAATCTCCTCTCAGCAA 60
aep.mel           TTCCGTGAGGACAAATATCATTTTGAGGGGCTACAGTCATTACTAATCTCCTCTCAGCAA 60
ore.ore           TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
add.nas           TACCATGAGGACAAATATCATTTTGAGGGGCAACAGTTATCACTAACCTTCTCTCAGCAA 60
ory.dam           TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTCCTCTCAGCAA 60
hip.equ           TGCCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAATCTCCTCTCAGCAA 60
alc.bus           TGCCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAATCTCCTCTCAGCAA 60
sig.lic           TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTCCTCTCAGCAA 60
bea.hun           TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACTAACCTCCTCTCAGCAA 60
dam.lun           TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCAACCTCCTCTCAGCAA 60
con.tau           TGCCATGAGGACAGATATCATTCTGAGGGGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
amm.ler           TGCCATGAGGACAAATATCATTTTGAGGGGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
pse.nay           TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACTAACCTTCTCTCAGCAA 60
cap.ibe           TACCATGAGGACAGATATCATTCTGAGGGGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
hem.jem           TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAATCTCCTCTCAGCAA 60
cap.fal           TACCATGAGGACAGATATCATTCTGAGGAGCAACAGTTATTACCAATCTCCTCTCAGCAA 60
rup.pyr           TACCATGAGGACAGATATCATTCTGGGGAGCAACAGTTATTACCAACCTCCTCTCAGCGA 60
rup.rup           TACCATGAGGACAGATATCATTCTGAGGGGCAACAGTTATTACCAATCTTCTCTCAGCAA 60
nem.cau           TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA 60
bud.tax.tax       TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTAATTACCAACCTCCTTTCAGCAA 60
pan.hod           TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCCTTTCAGCAA 60
ovi.amm          ,TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTCCTTTCAGCAA 60
ovi.vig           TACCATGAGGACAAATATCATTCTGAGGGGCTACAGTCATTACTAACCTCCTCTCAGCAA 60
cap.cri           TACCATGAGGACAAATATCATTCTGAGGAGCTACAGTCATCACTAACCTCCTCTCAGCAA 60
ovi.mos           TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATNACCAATCTCCTTTCAGCAA 60
ore.ame           TACCATGAGGACAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCCTCTCAGCAA 60
cep.dor           TCCCATGAGGGCAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCCTCTCAGCAA 60
cep.max           TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTCATTACCAACCTCCTATCAGCAA 60
bis.bon           TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATTACCAACCTCCTATCAGCAA 60
bos.gru           TACCATGAGGACAAATATCATTTTGAGGGGCAACAGTCATTACCAACCTCCTATCAGCAA 60
bos.tra           TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTTATTACCAATCTATTATCAGCAA 60
bub.min           TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
buba.bub          TGCCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
tra.ang           TGCCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATCACCAACCTCCTATCAGCAA 60
tra.eur           TGCCATGAGGACAAATATCATTCTGAGGAGCAACGGTCATCACAAACCTTCTATCAGCAA 60
kob.ell           TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 60
kob.meg           TACCATGAGGACAAATATCCTTCTGAGGAGCGACAGTCATCACTAATCTCCTTTCAGCAA 60
red.aru           TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAATCTTCTCTCAGCAA 60
red.ful           TGCCATGGGGACAAATATCCTTTTGAGGAGCAACAGTTATCACTAACCTTCTCTCAGCAA 60
neo.mos           TGCCATGGGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCAATCTACTATCAGCAA 60
pel.cap           TACCATGAGGACAAATATCCTTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
gaz.dam           TACCATGAGGACAAATATCTTTCTGAGGGGCAACAGTTATCACTAACCTCCTCTCAGCAA 60
our.our           TACCATGAGGACAAATATCCTTTTGAGGAGCAACAGTCATCACCAACCTCCTCTCAGCAA 60
ant.cer           TACCATGAGGACAAATATCTTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 60
sai.tat           TACCATGAGGACAAATATCTTTCTGAGGAGCAACAGTCATCACCAATCTCCTTTCAGCAA 60
mad.kir           TGCCATGAGGACAAATATCCTTCTGAGGAGCAACAGTTATCACTAACCTCCTCTCAGCAA 60
rap.mel           TACCATGGGGACAAATATCCTTTTGAGGAGCAACAGTCATCACTAATCTCCTCTCAGCAA 60
gaz.gaz           TACCATGAGGACAAATATCTTTCTGAGGAGCAACAGTTATCACGAACCTCCTCTCAGCAA 60
ant.ame           TACCATGAGGACAAATATCATTCTGAGGGGCAACAGTCATTATTAACCTACTCTCAGCAA 60
hyd.ine           TTCCATGAGGACAAATATCATTCTGAGGAGCAACGGTCATTACTAATCTCCTCTCAGCAA 60
mun.mun           TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATTATTAACCTCCTTTCAGCAA 60
alc.alc           TACCATGAGGACAGATATCATTTTGAGGGGCAACAGTTATTATTAACCTCCTTTCAGCAA 60
cer.eli kan       TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAACCTTCTCTCAGCAA
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cer.ela.xan     TACCATGAGGACAAATATCATTCTGAGGAGCAACGGTCATTACCAACCTTCTCTCAGCAA 60
cer.ela.can     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60
cer.nip.cent    TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA 60
cer.nip.yes     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA 60
cer.nip.ker     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60
cer.nip.pul     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTTCTCTCAGCAA 60
cer.nip.nip     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATTACCAACCTCCTCTCAGCAA 60
cer.ela.sco     TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACCAACCTTCTCTCAGCAA 60
cer.dam         TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60
ran.tar         TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTTATCACAAACCTCCTCTCAGCAA 60
mos.fus         TACCTTGAGGACAAATATCTTTCTGAGGAGCGACAGTTATTACCAATCTTCTCTCAGCAA 60
mos.leu         TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60
mos.chr         TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60
mos.ber         TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTTATTACCAATCTTCTCTCAGCAA 60
mos.mos         TACCTTGAGGACAAATATCTTTCTGAGGAGCAACAGTCATCACTAACCTTCTCTCAGCAA 60
tra.jav         TACCCTGAGGACAGATATCTTTCTGAGGAGCCACAGTCATCACCAACCTCTTATCAGCTA 60
trag.nap        TACCCTGAGGGCAAATATCTTTTTGAGGAGCTACAGTCATCACTAACCTTCTTTCAGCAA 60
bala.acu        TACCCTGAGGACAAATATCATTTTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60
bala.bon        TACCCTGAGGACAAATATCATTTTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA 60
bala.bor        TACCCTGAGGACAAATATCATTTTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
bala.edi        TACCCTGAGGACAAATATCATTTTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
esch.rob        TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAACCTCCTATCAGCAA 60
bala.mus        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA 60
mega.nov        TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTTCTATCAGCAA 60
bala.phy        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACTGTAATCACTAACCTCCTATCAGCAA 60
cap.mar         TGCCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAACCTCCTATCAGCAA 60
ceph.com        TACCCTGGGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
ceph.eut        TACCCTGGGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
lage.obl        TACCCTGAGGACAGATATCATTCTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
ceph.hea        TACCCTGAGGACAAATATCATTTTGAGGCGCAACAGTCATCACCAACCTCCTATCAGCAA 60
ceph.hec        TACCCTGAGGACAAATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
lage.aus        TACCCTGAGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
lage.cru        TACCCTGAGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
lage.obs        TACCCTGAGGACAGATATCATTTTGAGGTGCAACAGTCATCACCAACCTCCTATCAGCAA 60
lisso.bor       TACCCTGAGGGCAGATATCATTTTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60
lisso.per       TACCCTGAGGACAGATATCATTTTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60
glo.mac         TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60
glo.mel         TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60
fere.att        TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60
pepo.ele        TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60
gram.gri        TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCAGCAA 60
pse.cra         TACCCTGAGGACAGATATCATTCTGAGGCGCAACCGTCATCACCAATCTTCTATCAGCAA 60
lage.acu        TACCATGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAATCTCCTATCAGCAA 60
orci.bre        TACCCTGAGGACAGATATCTTTCTGAGGCGCAACCGTCATTACTAATCTCCTATCAGCAA 60
orca.bre        TACCCTGAGGACAGATATCCTTCTGAGGTGCAACCGTCATCACCAATCTCCTATCAGCAA 60
del.cap         TGCCCTGGGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
del.tro         TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
del.del         TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
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sten.coe        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
tur.adu         TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
sten.fro        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
saus.chi        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATCACCAACCTCCTATCAGCAA 60
sten.lon        TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCAGCAA 60
turs.tru        TGCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAACCTCTTATCAGCAA 60
lage.alb        TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACTAATCTCCTATCAGCAA 60
sten.bre        TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATTACCAACCTCCTGTCAGCAA 60
sota.flu        TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATTACCAATCTCCTATCAGCAA 60
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del.leu	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATTACCAATCTCCTATCAGCAA	60
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plat.min	TACCCTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTTTTATCAGCAA	60
kogi.bre	TACCCTGAGGCCAAATATCATTCTGAGGAGCAACCGTCATCACCAACCTTATATCCGCAA	60
kogi.sim	TGCCCTGAGGCCAAATATCATTCTGAGGAGCAACCGTCATCACAAACCTTATATCCGCAA	60
phys.cat	TGCCCTGAGGACAAATATCATTCTGAGCCGCAACCGTTATCACAAACCTTCTATCAGCAA	60
lipo.vex	TACCCTGAGGACAAATATCATTTTGAGGCGCAACCGTCATCACTAATCTTCTATCAGCAA	60
phoc.sin	TGCCCTGGGGACAAATATCATTTTGAGGTGCTACCGTCATCACAAACCTCTTATCAGCAA	60
bera.bai	TGCCTTGAGGGCAAATATCATTCTGAGGTGCAACCGTCATCACCAACCTCCTATCCGCTA	60
ziph.car	TACCTTGAGGACAAATATCATTCTGAGGTGCAACCGTCATCACAAACCTCTTATCCGCTA	60
meso.eur	TTCCCTGAGGACAAATATCATTCTGAGGCGCAACCGTTATTACCAACCTCCTATCCGCCA	60
meso.bid	TACCCTGAGGACAAATATCATTCTGAGGCGCAACTGTTATTACTAACCTCCTATCCGCTA	60
meso.den	TACCATGAGGACAAATATCCTTCTGAGGTGCAACTGTCATTACCAATCTTCTATCCGCTA	60
hype.amp	TACCCTGAGGACAAATATCATTCTGAGGCGCAACCGTCATCACCAATCTCCTATCCGCCA	60
meso.per	TACCTTGAGGACAAATATCATTCTGAGGCGCAACTGTCATTACTAATCTTTTATCTGCTA	60
pont.bla	TACCCTGAGGACAAATGTCATTCTGAGGTGCCACTGTCATCACTAACCTCCTATCAGCGA	60
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dic.sum	TACCATGAGGTCAAATATCCTTCTGAGGAGCCACAGTTATCACAAATCTCCTCTCAGCCA	60
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cera	TACCATGAGGCCAAATATCCTTCTGAGGGGCTACAGTCATCACAAACCTCCTCTCAGCTA	60
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phac.afr	TACCCTGAGGACAAATATCGTTCTGAGGAGCCACAGTCATCACAAACCTACTATCAGCCA	60
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sus.scr.ewb3	TGCCCTGAGGACAAATATCATTCTGAGGAGCTACGGTCATCACAAATCTACTATCAGCTA	60
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zal.cal	TTCCATGAGGACAAATATCATTTTGAGGAGCAACCGTCATTACCAACCTCCTATCAGCAG	60
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pho.fasciata	TACCATGAGGACAAATATCATTCTGAGGAGCAACAGTCATCACTAATCTACTATCAGCAA	60
pho.gro	TACCATGAGGGCAAATGTCATTCTGAGGAGCAACAGTTATCACTAATCTACTATCAGCAA	60
pho.vit	TACCATGAGGACAAATATCATTTTGAGGAGCAACAGTCATCACCAATCTACTATCAGCAA	60
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sel.thi	TACCCTGAGGCCAAATATCCTTCTGAGGAGCGACTGTCATTACCAACCTCCTATCAGCCA	60
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can	TACCATGAGGACAAATATCATTTTGAGGAGCAACTGTAATCACTAATCTTCTCTCTGCCA	60
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oto.gar        TCCCATGAGGACAAATGTCATTCTGAGGCGCAACCGTAATTACAAATCTCCTCTCAGCAA 60
lor.tar        TCCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATTACCAACCTACTATCAGCAA 60
nyc.cou        TCCCATGAGGACAAATATCATTCTGAGGTGCCACCGTCATCACTAACCTACTATCGGCAA 60
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gorr           TCCCATGAGGCCAAATATCCTTCTGAGGAGCCACAGTAATCACAAACTTGCTATCCGCCA 60
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fra.fra        TCCCATGAGGCCAAATATCATTCTGAGGGGCTACCGTCATTACGAACCTATTCTCAGCAA 60
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gru.leu        TACCATGAGGACAAATATCATTTTGAGGGGCTACAGTCATTACCAACCTCTTCTCAGCCG 60
gru.can.pra    TGCCATGAGGACAAATATCATTCTGAGGGGCTACAGTCATTACCAACCTCTTCTCAGCCG 60
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fal.spa        TACCCTGAGGACAAATGTCATTCTGAGGAGCCACAGTCATTACCAACCTATTCTCAGCAA 60
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vid.cha        TGCCATGAGGACAAATATCATTCTGAGGAGCCACAGTAATCACAAACCTATTCTCAGCAA 60
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bud.tax.tax	TCCCATACATTGGCACAAACCTAGTTGAGTGAATCTGAGGAGGATTCTCAGTAGACAAAG	120
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red.aru	TCCCATACATCGGCACAAACCTAGTCGAATGAATCTGAGGAGGATTCTCAGTCGATAAAG	120
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mos.chr           TTCCTTACATTGGTACTAATCTGGTTGAATGAATCTGAGGAGGCTTCTCAGTAGACAAAG 120
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tur.adu           TCCCTTATATTGGCACTACCTTAGTAGAATGAATCTGAGGTGGATTCTCCGTAGACAAAG 120
sten.fro          TCCCTTACATTGGCACTACCTTAGTTGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG 120
saus.chi          TCCCTTATATTGGCACTACCCTAGTTGAATGAATCTGAGGTGGATTTTCCGTAGACAAAG 120
sten.lon          TCCCTTATATCGGCACTACCTTAGTCGAATGAATCTGAGGTGGATTTTCCGTAGACAAAG 120
turs.tru          TCCCTTATATCGGTACTACCCTAGTAGAATGAATCTGAGGTGGATTCTCCGTAGACAAAG 120
lage.alb          TCCCTTACATCGGCACTACCTTGGTAGAATGAATCTGAGGCGGATTTTCCGTAGACAAAG 120
sten.bre          TCCCTTACATCGGCACTACCTTAGTAGAATGAATCTGAGGCGGATTCTCCGTAGACAAAG 120
sota.flu          TCCCTTACATCGGTAACACCTTAGTAGAATGAATCTGAGGTGGGTTCTCCGTAGACAAAG 120
del.leu           TCCCTTACATCGGCAACACCTTAGTAGAATGAATCTGAGGTGGGTTTTCTGTAGATAAAG 120
mono.mon          TCCCTTATATCGGCAGTACCCTAGTCGAGTGAATCTGAGGTGGCTTTTCCGTAGATAAAG 120
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plat.min          TTCCTTATATCGGCACTACCCTAGTAGAATGAGTTTGAGGTGGCTTCTCCGTAGACAAAG 120
kogi.bre          TTCCTTACATCGGCACTACCCTAGTGGAATGAGTTTGAGGTGGTTTCTCCGTGGACAAAG 120
kogi.sim          TCCCTTACATCGGCACTACCCTAGTAGAGTGAGTTTGAGGTGGTTTCTCCGTAGATAAGG 120
phys.cat          TTCCCTATATCGGCACCACCCTAGTAGAGTGAGTTTGAGGTGGATTTCTCAGTAGACAAAG 120
lipo.vek          TTCCTTACATCGGAACTACCTTAGTAGAGTGAGTTTGAGGTGGATTTCTCCGTAGACAAAG 120
phoc.sin          TTCCTTACATCGGCAGTACCCTAGTGGAGTGAATTTGAGGTGGATTTCTCCGTAGACAAAG
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bera.bai      TTCCTTATATCGGCACCACTCTTGTCGAATGAATCTGAGGTGGCTTCTCCGTAGATAAAG 120
ziph.car      TCCCCTATATCGGCACTACTCTAGTCGAATGAATCTGAGGTGGTTTTTCAGTAGATAAAG 120
meso.eur      TCCCCTATATTGGCACTACTCTAGTCGAATGAATCTGAGGTGGCTTTTCCGTAGATAAAG 120
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hype.amp      TTCCCTATATCGGCACTACCCTAGTTGAATGAATCTGAGGTGGTTTCTCCGTAGACAAAG 120
meso.per      TCCCTTATATTGGCACCACCCTAGTTGAATGAATTTGAGGTGGCTTCTCCGTAGATAAAG 120
pont.bla      TCCCCTACATCGGAACTACCCTTGTAGAATGGATCTGAGGTGGTTTCTCTGTAGACAAAG 120
hex.lib       TCCCCTACATTGGAACAGACCTAGTAGAATGAATCTGAGGAGGCTTTTCTGTAGATAAAG 120
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rhin.son      TCCCCTATATCGGTACCAACCTTGTAGAGTGAATCTGAGGAGGATTCTCAGTCGACAAAG 120
cera          TCCCTTACATCGGCACCAACCTCGTAGAATGAATCTGAGGAGGATTTTCCGTTGACAAAG 120
equu          TCCCCTACATCGGTACTACGCTCGTCGAATGAATCTGAGGTGGATTCTCAGTAGACAAAG 120
baby.bab      TTCCCTATATCGGAACGGACCTCGTAGAATGGATCTGAGGAGGCTTCTCCGTCGATAAAG 120
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sus.bar       TCCCCTATATCGGAACAGACCTCGTAGAATGAATCTGAGGGGGCTTTTCCGTCGACAAAG 120
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lama.gua      TTCCATATGTTGGCACAACACTAGTCGAATGAATTTGAGGGGGTTCTCCGTAGATAAAG 120
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cam.bac       TTCCCTATATCGGCACAACACTAGTAGAATGAATTTGAGGTGGCTTCTCCGTAGACAAAG 120
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arc.gaz       TCCCCTACATCGGAACTAACCTAGTAGAATGAATCTGAGGAGGATTTTCAGTTGATAAGG 120
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zal.cal       TCCCTTACATCGGAACCAACCTAGTAGAATGAATTTGAGGGGGATTTTCAGTCGACAAAG 120
odo.ros       TTCCCTATGTAGGGACTGACTTGGTCGAATGAGTCTGAGGGGGGTTTTCAGTTGATAAAG 120
pho.fasciata  TTCCCTATATCGGAACCGACCTAGTACAATGAATCTGAGGAGGATTTTCAGTTGATAAAG 120
pho.gro       TCCCCTACATCGGAACCGATCTAGTACAATGAATCTGAGGAGGGTTCTCAGTTGATAAAG 120
pho.vit       TCCCCTATGTCGGAACCGACCTTGTACAATGAATCTGAGGAGGGTTTTCAGTAGATAAAG 120
cys.cri       TCCCCTACATCGGAGCCGATCTAGTAGAATGAATCTGAGGGGGATTTTCAGTCGATAAAG 120
hyd.lep       TTCCCTACATCGGAACCGACCTAGTACAATGAATTTGAGGCGGATTTTCAGTCGACAAAG 120
lep.wed       TTCCCTACATCGGAACTGACTTAGTACAATGAATCTGAGGCGGATTTTCAGTTGACAAAG 120
mir.leo       TCCCCTATGTCGGAGACGACCTAGTACAATGAATCTGAGGAGGATTTTCAATCGACAAAG 120
eri.bar       TCCCCTACATCGGGACTGATCTAGTACAATGAATCTGAGGAGGATTCTCAGTTGACAAAG 120
mon.sch       TCCCTTACATCGGAACCGATCTAGTACAATGAATCTGAGGCGGTTCTCAGTAGATAAAG 120
hela.mal      TCCCCTATATTGGAACGGACCTAGTAGAATGAGTCTGAGGAGGCTTTTCCGTAGACAAGG 120
sel.thi       TCCCCTATATTGGAACAGACCTAGTAGAATGAATCTGAGGGGGCTTTTCTGTAGATAAAG 120
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cal           TTCCTTACATCGGTACAGACTTAGTAGAATGAATTTGAGGTGGGTTCTCAGTAGACAAAG 120
gla.sab       TTCCTTATATTGGGACAACACTTGTAGAATGAATCTGAGGAGGCTTCTCTGTCGACAAAG 120
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hyl.pha       TCCCCTACATTGGAACAGTCCTTGTCGAATGAATTTGAGGGGGATTTTCCGTAGATAAGG 120
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bel.pea       TCCCTTATATTGGAACTGATCTAGTAGAGTGAATCTGAGGGGGGTTTTCAGTTGACAAGG 120
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gala.demi     TCCCATATATAGGGCCTACTCTAGTAGAATGAATCTGAGGGGGGTTTTCGGTAGACAAAG 120
pero.pot      TCCCATATGTAGGTACAACCCTGGTAGAATGAATTTGAGGGGGATTCTCAGTAGACAAAG 120
gala.mat      TTCCTTACATGGGTACCGGCCTAGTAGAATGAATCTGAGGGGGATTTTCAGTAGACAAAG 120
gala.moh      TTCCCTATATAGGAACTGGCCTAGTAGAATGAATTTGAGGAGGGTTCTCAGTAGACAAAG 120
oto.gar       TTCCCTACATAGGAACTAACCTAGTAGAGTGAATCTGAGGGGGATTTTCAGTAGACAAAG 120
lor.tar       TTCCTTACATCGGAACTAACCTAGTTGAATGAATCTGAGGGGGGTTCTCAGTAGATAAAG 120
nyc.cou       TTCCCTATATTGGCACAAACCTAGTTGAATGGGTCTGAGGAGGCTTTTCAGTAGATAAAG 120
mus           TCCATATATTGGAACAACCCTAGTCGAATGAATTTGAGGGGGTTTTCAGTAGACAAAG 120
gorg          TCCCTTACATCGGAACAGACCTAGTCCAATGAGTTTGAGTTTTTTATTCAGTAGATAGCC 120
homo          TCCTATACATTGGACAGACCTAGTTTAATGAATTTGAGGAGGTTATTCAGTAGACAGTT 120
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dug.dug          TCCCCTACATCGGCACCAACCTAGTCGAATGAGTTTGAGGGGGATTCTCAGTAGACAAAG 120
ele.max          TTCCCTACATCGGCACAAACCTAGTAGAATGAATTTGAGGAGGCTTTTCGGTAGATAAAG 120
afr.con          TCCCCTATATTGGTCAAACCCTAGTAGAATGGGCCTGAGGAGGATTCTCAGTTGACAACC 120
pavo.mut         TCCCTTATATTGGACAAACCCTAGTAGAATGAGCCTGAGGGGGATTCTCAGTCGACAACC 120
tra.bly          TCCCATACATTGGCCAAACCTTAGTAGAATGAGCCTGAGGAGGCTTTTCAGTTGACAATC 120
tra.sat          TCCCATACATTGGTCAAACCCTAGTAGAATGAGCGTGAGGCGGCTTTTCAGTTGACAATC 120
tra.cob          TCCCATACATTGGCCAAACTCTAGTAGAATGGGCCTGAGGGGGCTTTTCAGTTGACAATC 120
tra.tem          TCCCATACATTGGCCAAACCCTAGTAGAATGAGCTTGAGGGGGCTTTTCAGTTGACAATC 120
arg.arg          TCCCTTATATTGGACAAACCCTAGTAGAGTGAGCCTGAGGAGGATTTTCAGTCGACAACC 120
cat.wal          TCCCTTACATCGGACAGACCCTAGTAGAATGAGCCTGAGGAGGATTCTCAGTTGACAATC 120
cro.cro          TCCCTTACATTGGACAAACCCTAGTCGAGTGAGCCTGAGGGGGATTCTCAGTTGACAACC 120
sym.ree          TCCCCTACATCGGACAAACCCTAGTAGAGTGGGCCTGAGGAGGATTCTCAGTTGACAACC 120
bam.tho          TTCCCTACATCGGACAAACCCTAGTAGAATGAGCCTGGGGGGGATTCTCAGTAGACAACC 120
fra.fra          TTCCCTACATTGGACAAACCTTAGTAGAGTGAGCCTGAGGGGGATTCTCAGTAGATAACC 120
ith.cru          TTCCCTACATCGGCCAAACTCTGGTAGAATGAGCTTGAGGAGGATTTTCAGTAGACAACC 120
ant.par          TCCCATATATCGGCCAAACCCTTGTAGAATGAGCTTGAGGGGGTTTCTCAGTAGACAATC 120
ant.vir          TCCCATACATCGGCCAAACCCTTGTAGAATGAGCTTGAGGGGGTTTTTCAGTAGATAATC 120
gru.ant.ant      TCCCCTACATCGGCCAAACCCTTGTAGAATGAGCTTGAGGGGGCTTCTCAGTAGACAATC 120
gru.ant.gil      TCCCCTACATCGGCCAAACCCTTGTAGAATGAGCTTGAGGGGGCTTCTCAGTAGACAATC 120
gru.ant.sha      TCCCCTACGGCGGCCAAACCCTTGTAGAATGAGCTTGAGGGGGCTTCTCAGTAGACAACC 120
gru.leu          TCCCCTACATCGGCCAAACCCTTGTAGAATGAGCTTGAGGGGGCTTCTCAGTAGACAATC 120
gru.can.pra      TCCCATACATCGGCCAAACCCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAATC 120
gru.can.row      TCCCATACATCGGCCAAACCCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAATC 120
gru.can.tab      TCCCATACATCGGCCAAACCCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAATC 120
gru.can.can      TCCCATACATCGGCCAAACCCTCGTAGAATGGGCTTGAGGGGGCTTCTCAGTAGACAATC 120
gru.ame          TCCCATACATCGGCCAAACCATCGTAGAATGAGCTTGAGGGGGCTTCTCTGTAGACAACC 120
gru.gru          TCCCATACATCGGCCAAACCCTCGTAGAATGAGCTTGAGGGGGCTTCTCAGTAGACAACC 120
gru.mon          TCCCATACATCGGCCAAACCCTCGTAGAATGAGCTTGAGGAGGCTTCTCAGTAGACAACC 120
gru.nig          TCCCATACATCGGCCAAACCCTCGTAGAATGAGCTTGAGGAGGCTTCTCAGTAGACAACC 120
gru.jap          TCCCATACATCGGCCAAACCCTCGTAGAATGAGCTTGAGGGGGCTTCTCAGTAGACAACC 120
cic.boy          TCCCCTACATCGGCCAAACCCTCGTAGAATGGGCCTGAGGGGGCTTCTCCGTCGATAACC 120
rhe.ame          TCCCGTACATCGGACAAACCTTGGTAGAATGAGCTTGAGGGGGGTTTCAGTAGACAACC 120
ant.alb          TCCCATACATCGGCCAAACCTTAGTAGAATGGGCCTGAGGGGGATTCTCCGTTGACAACC 120
fal.fam          TCCCATACATCGGTCAAACCCTAGTCGAGTGGGCCTGAGGAGGATTTTCAGTAGACAATC 120
fal.ver          TCCCATACATCGGCCAAACCCTAGTCGAATGGGCCTGAGGAGGATTTTCAGTAGATAACC 120
fal.per          TCCCATACATCGGCCAAACCCTAGTCGAATGAGCTTGAGGGGGATTTTCAGTAGACAACC 120
fal.spa          TCCCATATATCGGCCAAACCCTAGTCGAATGGGCCTGAGGAGGATTCTCAGTAGACAACC 120
ayt.ame          TCCCATACATCGGGCAAACCCTTGTAGAATGGGCCTGAGGAGGATTCTCGGTAGACAACC 120
smi.sha          TTCCATACATCGGACAAACCCTAGTAGAATGAGCTTGGGGAGGATTTTCAGTAGACAACC 120
vid.cha          TTCCATACATTGGCCAAACCCTAGTAGAATGAGCCTGAGGAGGATTCTCAGTAGACAACC 120
chry.pic         TCCCATTCATTGGTAACACATTAGTACAATGAATCTGAGGTGGATTCTCAGTAGACAACG 120
emy.orb.kur      TCCCATACATTGGCAATACACTAGTGCAATGAATCTGAGGGGGATTCTCAGTAGATAACG 120
che.mud          TCCCATACATCGGCAACACACTAGTACAATGAATCTGAGGAGGGTTTTCAGTAGACAATG 120
eum.egr          TTCCATACATTGGCACCAACCTAGTAGAATGAATTTGAGGGGGCTTTTCCGTAGACAACG
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aep.mel          CAACCCTNACCCGATTTTTCGGYTTCCACTTCATCYTTCCATTCATCATTGCGGCACTAG 180
ore.ore          CAACCCTTACCCGATTCTTTGCCTTCACTTCATCTTTCCATTTATCATCGCAGCCCTAG 180
add.nas          CAACCCTTACCCGATTTTTCGCCTTCCACTTTATTCTCCCCTTTATTATCGCTGCCCTTP 180
ory.dam          CAACCCTCACCCGATTTTTCGCCTTCCACTTTATTCTCCCTTTTATTATCGCTGCCCTTG 180
hip.equ          CAACCCTCACCCGATTCTTCGCCTTCCACTTTATTCTTCCCTTTATCATCATTGCCCTTG 180
alc.bus          CAACCCTTACCCGATTTTTTGCCTTCCACTTCATTCTTCCATTCATCATTGCAGCCCTTG 180
sig.lit          CAACCCTTACCCGATTTTTTGCCTTCCACTTCATTCTCCCATTCATCATTGCAGCCCTTG 180
bea.hun          CAACCCTCACCCGATTTTTCGCTTTCCACTTTATTCTCCCATTTATCATTACAGCCCTTG 180
dam.lun          CGACCCTCACCCGATTTTTTGCTTTCCACTTCATTCTCCCATTTATCATCGTAGCTCTTG 180
ton.tau          CAACCCTTACCCGATTTTTCGCCTTCCACTTCATTCTCCCATTTATCATTACAGCCCTTG 180
amm.lec          CTACTTTCACCCGATTTTTCGCTTTCCATTTCATTCTCCCATTTTAATTTCAGCCCTAG 180
pse.nay          CTACTCTCACCCGATTTTTCGCTTTCCACTTCATTCTCCCATTTATTATTATAGCCCTTG
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hem.jem	CCACCCTCACCCGATTCTTCGCCTTCCACTTTATCCTCCCATTCATCATTGCAGGCCTCG	180
cap.fal	CTACCCTCACCCGATTCTTTGCCTTTCACTTCATCCTCCCATTCATCATTGCAGCCTTAG	180
rup.pyr	CTACCCTCACCCGATTCTTTGCCTTCCACTTCATCCTCCCATTTATCATTGCAGCCTTAG	180
rup.rup	CTACCCTCACCCGATTCTTTGCCTTCCACTTCATCCTCCCATTTATCATTACAGCTACTG	180
nem.cau	CTACTCTCACCCGATTCTTCGCCTTCCACTTCATCCTCCCATTTATCATCGCAGACCTCG	180
bud.tax.tax	CATCCCTCACCCGATTCTTTGCCTTTCACTTCATCCTCCCATTCATCATCGCAGCCCTCG	180
pan.hod	CTACCCTTACCCGATTCTTTGCCTTCCATTTCATTCTCCCATTCATCATCGCAGCCCTCG	180
ovi.amm	CCACCCTGACCCGATTCTTCGCCTTTCACTTTATTTTCCCATTCATCATCGCAGCCCTCG	180
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ovi.mos	CCACCCTCACCCGATTTTTTGCTTTTCACTTTATCCTCCCATTTATCATCGTAGCCCTCG	180
ore.ame	CTACCCTCACCCGATTTTTCGCCTTCCACTTCATTCTCCCATTTATCATCGCAGCCCTCG	180
cep.dor	CAACTCTCACCCGATTCTTTGCTTTCCACTTTATCTTCCCTTTTATTATTGCAGCCCTCG	180
cep.max	CAACCCTCACTCGATTTTTCGCCTTCCACTTTATCTTCCCATTTATCATCGCAGCCCTTG	180
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bos.gru	CAACCCTCACCCGATTCTTCGCTTTCCACTTTATCCTCCCATTTATTATTACAGCAATTG	180
bos.tra	CAACCCTAACCCGATTCTTCGCTTTCCACTTTATCCTCCCATTCATCATTGCAGCCCTCG	180
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buba.bub	CAACCCTCACCCGATTCTTCGCATTTCACTTCATCCTCCCATTCATTATCGCAGGACTTG	180
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red.aru	CAACCCTTACCCGATTCTTCGCCTTCCACTTTATCCTCCCATTTATCATCATAGCCCTCG	180
red.ful	CAACCCTCACTCGATTCTTCGCCTTCCACTTTATCCTCCCATTTATCATCGCAGCACTCG	180
neo.mos	CAACCCTCACCCGATTTTTTGCCTTCCACTTCATTCTCCCATTTATCATTGCAGCCCTCA	180
pel.cap	CAACCCTCACCCGATTTTTTGCTTTCCACTTTATTCTCCCATTTATCATTGCAGCCCTTG	180
gaz.dam	CAACACTCACCCGATTCTTTGCCTTCCATTTCATCTTCCCATTCATCATTGCAGCCCTTG	180
our.our	CAACTCTAACCCGATTCTTTGCCTTCCACTTCATCCTCCCATTTATCATTGCAGCCCTTA	180
ant.cer	CAACCCTTACCCGATTTTTCGCCTTCCACTTTATCCTCCCATTTATTATCGCAGCTCTCG	180
sai.tat	CAACCCTCACCCGATTCTTCGCCTTCCACTTCATCCTCCCATTCATTATTGCAGCCCTAG	180
mad.kir	CAACCCTCACCCGATTCTTCGCCTTCCATTTTATTCTCCCATTCATTATCGCAGCCCTAG	180
rap.mel	CAACCCTCACCCGATTCTTCGCTTTTCACTTCAGTTCTCCATTTATCATTGCAGCCCTCG	180
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hyd.ine	CTACCCTGACCCGATTCTTCGCCTTCCACTTCATTCTTCCATTTATCATTGCAGCACTTG	180
mun.mun	CAACCCTCACCCGATTCTTTGCCTTCCACTTTATCCTCCCATTTATTATTGCAGCACTTG	180
alc.alc	CAACTCTAACCCGATTTTTCGCCTTCCACTTTATTCTCCCATTTATCATCGCAGCACTTG	180
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cer.ela.sto	CAACCCTAACCCGATTTTTCGCTTTCCACTTTATTCTCCCATTTATCATCGCAGCACTCG	180
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mos.chr	CAACACTCATTCGATTCTTTGCCTTTCATTTCATTCTTCCATTTATCATCGTAGCACTCG	180
mos.ber	CAACACTCATCCGATTCTTTGCCTTTCATTTTATTCTTCCATTTATCATTGCAGCATTCG	180
mos.mos	CAACACTCATCCGATTCTTTGCCTTTCATTTTATTCTTCCATTTATCATTACAGCCCTAG	180
tra.jav	CAACCCTTACACGATTCTTTGCCTTTCATTTCATTCTTCCATTTGTTATTACAGCCCTAG	180
trag.nap	CAACCCTTACACGATTTTTTGCCTTTCATTTCATTCTTCCATTTATTATCCTAGCATTAG	180
sala.atu	CAACATTAACACGTTTTTTTGCCTTTCATTTTATTCTTCCCTTTTATTATTCTAGCATTAG	

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bala.bor	CAACACTAACACGCTTTTTTGCCTTCCACTTCATTCTCCCCTTCATTATTCTAGCACTAG	180
bala.edi	CAACACTAACACGCTTTTTTGCCTTCCACTTTATCCTCCCCTTCATTATCCTAGCACTAG	180
esch.rob	CAACACTAACACGCTTCTTTGCCTTCCACTTCATCCTTCCATTCATTATCCTAGCACTAG	180
bala.mus	CAACACTAACACGCTTCTTTGCCTTCCACTTCATTCTCCCCTTCATCATTATAGCATTAG	180
mega.nov	CAACACTAACACGTTTCTTTGCTTTCCACTTCATCCTCCCCTTCATCATTACAGCATTAG	180
bala.phy	CAACACTAACACGCTTTTTTGCCTTTCACTTTATCCTCCCCTTCATCATCCTAGCATTAG	180
cap.mar	CGACACTAACTCGCTTCTTTGCTTTCCACTTCATCCTCCCTTTCATTATTCTAGCGCTAG	180
ceph.com	CAACACTAACACGCTTTTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCATTAG	180
ceph.eut	CAACACTAACACGCTTTTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCATTAG	180
lage.obl	CAACACTAACACGCTTTTTCGCTTTCCACTTTATCCTCCCATTCATCATCACAGCATTAG	180
ceph.hea	CAACACTAACACGCTTTTTCGCCTTCCACTTTATCCTCCCATTCATCATCACAGCATTAG	180
ceph.hec	CAACACTAACACGCTTTTTCGCCTTTCACTTTATCCTCCCATTCATCATCACAGCATTAA	180
lage.aus	CAACACTAACACGCTTTTTCGCTTTCCACTTTATCCTCCCATTCATCATCACAGCATTAG	180
lage.cru	CAACACTAACACGCTTTTTCGCTTTCCACTTCATCCTCCCATTCATCATCACAGCATTAG	180
lage.obs	CAACACTAACACGCTTTTTCGCTTTCCACTTTATCCTCCCATTCATCATCACAGCATTAG	180
lisso.bor	CAACACTAACACGCTTTTTCGCTTTCCACTTTATCCTCCCATTCATCATCACAGCATTAG	180
lisso.per	CAACACTAACACGCTTTTTCGCTTTCCACTTTATCCTCCCATTCATCATCACAGCATTAG	180
glo.mac	CAACACTAACACGTTTTTTCGCTTTCCACTTTATCCTCCCATTCATCATCACAGCATTAG	180
glo.mel	CAACACTAACACGTTTTTTCGCTTTCCACTTTATCCTCCCATTCATCATCACAACATTAG	180
fere.att	CAACACTAACACGTTTTTTCGCTTTCCACTTTATCCTCCCATTCATCATCACAGCATTAG	180
pepo.ele	CAACACTAACACGTTTTTTCGCTTTCCACTTCATCCTCCCATTCATCATCACAGCATTGG	180
gram.gri	CAACACTAACACGCTTTTTCGCTTTCCACTTTATCCTCCCATTCATCATCACAGCATTAG	180
pse.cra	CAACACTAACACGTTTTTTCACTCTCCACTTTATCCTCCCATTCATCATTACAGCACTAA	180
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orci.bre	CAACACTAACACGTTTCTTTGCCTTCCACTTTATCCTCCCATTCATCATCACAGCATTAA	180
orca.bre	CAACACTAACACGTTTTTTCGCCTTCCACTTTATCCTTCCATTCATCATCACAGCACTAG	180
del.cap	CAACATTAACACGCTTTTTCGCTTTCCACTTTATCCTTCCATTCATCATCACAGCATTAG	180
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del.del	CAACATTAACACGCTTTTTCGCTTTCCACTTTATCCTCCCATTCATCATCACAGCACTAG	180
sten.cly	CAACATTAACACGCTTTTTCGCTTTCCACTTTATCCTCCCGTTCATCATCACAGCATTAG	180
sten.coe	CAACATTAACACGCTTTTTCGCTTTCCACTTTATCCTCCCGTTCATTATCACAGCATTAG	180
tur.adu	CAACACTAACACGCTTTTTCGCTTTCCACTTTATCCTCCCGTTCGTCATCACAGCATTAG	180
sten.fro	CAACATTAACACGCTTTTTCGCTTTCCACTTTATCCTCCCGTTCATCATCACAGCATTAG	180
saus.chi	CAACATTAACACGCTTTTTCGCTTTCCACTTTATCTTTCCCTTCATCATCACAGCATTAG	180
sten.lon	CAACATTAACACGCTTTTTCGCTTTCCATTTTATCCTCCCATTCATCATCACAGCATTAG	180
turs.tru	CAACATTAACACGCTTTTTCGCCTTCCACTTTATTCTTCCATTCATCATCACAGCATTGG	180
lage.alb	CAACACTAACACGCTTCTTCGCTTTCCACTTTATCCTCCCATTCATCATCACAGCACTAG	180
sten.bre	CAACACTAACACGTTTTTTCGCTTTCCACTTTATCCTCCCATTCATCATCATAGCATTAG	180
sota.flu	CAACACTAACACGCTTTTTCGCCTTCCACTTTATCCTCCCATTTATCATCACAGCATTAG	180
del.leu	CAACACTAACACGCTTCTTCACCTTCCACTTTATCCTCCCATTCATCATTACAGCGCTAG	180
mono.mon	CAACACTAACACGCTTCTTCACCTTCCACTTTATCCTCCCATTCATCATCACAGCACTAG	180
plat.gan	CAACACTAACACGATTCTTTGCCTTTCACTTCATCCTCCCTTTCATCATCCTAACACTAG	180
plat.min	CAACACTAACACGATTCTTTGCCTTTCACTTCATCCTCCCTTTCATCATCCTAACACTAG	180
kogi.bre	CCACATTAACACGCTTCTTTGCCTTTCACTTCATCCTCCCCTTTATCATCCTAGCACTGG	180
kogi.sim	CTACGCTAACACGCTTCTTTGCTTTCCACTTTATTCTCCCCTTCATCATCCTAGCACTAG	180
phys.cat	CAACACTGACACGCTTCTTCACTCTCCACTTCATCCTCCCCTTTATCACCCTAACACTAA	180
lipo.vex	CAACATTAACCCGCTTCTTCGCTCTCCATTTCATCCTTCCATTTATTATTGTAGCACTAA	180
phoc.sin	CAACACTAACACGCTTCTTCGCCTTCCATTTTATCCTTCCATTTATCATTACAGCACTAA	180
bera.bai	CTACACTAACACGCTTCTTTGCCTTCCATTTTATCCTCCCTTTTATCATTCTAACCCTAG	180
ziph.cav	CCACACTAACACGCTTCTTTGCCTTCCATTTCATCCTTCCATTTATTATTTTAGCCCTAG	180
meso.eur	CTACACTAACACGCTTCTTTGCTTTTCATTTTATCCTTCCATTCATTATTCTAGCCCTAA	180
meso.bid	CTACATTAACACGCTTCTTTGCTTTTCATTTTATCCTTCCATTTATTATTTTAGCCCTAG	180
meso.den	CTACATTAACACGCTTCTTTGTTTTTCATTTATCCTTCCTTTTATTATTCTAGCCCTAA	180
hype.amp	CTACATTAACCCGCTTTTTTGTCCTTCCATTTTATCCTTCCATTCATTATTCTAGCCCTAG	180
meso.per	CTACATTAACACGATTTTTTGCCTTCCATTTTATTCTTCTATTTATTATCTTAGCTCTAA	180
pont.bla	TAACACTAACGCGATTCTTTGTTTTTCATTTTATTCTTTCATTCATTATTACAGCCCTAG	180
hex.lib	CGACCCTTACACGATTCTTTGCTTTTCATTTTATTCTTTCATTCATTATCATAGCACTAG	180

hipp.amp	CCACCCTTACACGATTCTTTGCCTTCCACTTTATTCTTCCATTCGTTATCACAGCACTAG	130
dic.sum	CCACCCTCACCCGGTTCTTTGCTTTCCACTTCATCCTCCCCTTCATCATCCTAGCCCTAG	130
rhin.son	CTACCCTTACCCGATTCTTTGCCTTCCACTTCATCCTTCCCTTTATTATCCTAGCTCTAG	130
cera	CCACACTTACACGATTCTTCGCCTTTCACTTTATCCTCCCCTTTATTATCATAGCCCTAG	130
equu	CCACCCTTACCCGATTTTTTGCCTTCCACTTTATTCTACCCTTTATCATCACAGCCCTGG	130
baby.bab	CAACCCTCACACGATTCTTTGCTTTCCACTTTATTCTACCCTTCATCATCACCGCTCTCG	130
phac.afr	CAACTCTCACACGATTCTTTGCCTTCCACTTCATTTTACCTTTTATCATCGCTGCCCTAG	130
sus.bar	CAACCCTTACACGATTCTTCGCCTTTCACTTTATCCTGCCCTTCGTCATTACCGCCCTCG	130
sus.scr.ewb3	CAACCCTCACACGATTCTTCGCCTTCCACTTTATCCTGCCATTCATCATTACCGCCCTCG	130
lama.gla	CCACCCTTACACGATTCTTCGCCTTCCACTTTATCTTACCTTTTGTCATTGCAGCTCTAG	130
lama.gua	CCACCCTTACRCGATTCTTCGCCTTCCACTTTATCTTACCTTTTGTCATTGCAGCTCTAG	130
vic.vic	CCACCCTTAACCGATTCTTCGCCTTTCACTTTATCTTACCTTTCATCATTGCAGCTCTAG	130
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arc.for	CAACCCTAACACGATTCTTCGCCTTTCACTTCATTCTCCCCTTCGTAGCATCAGCACTAG	130
arc.gaz	CAACCCTAACACGATTCTTCGCCTTTCACTTTATTCTTCCCTTCGTAGTATCAGCACTAG	130
eum.jub	CAACCCTAACACGATTCTTCGCCTTCCACTTTATTCTCCCCTTCGTAGCATCAGCACTAG	130
zal.cal	CAACCCTAACACGATTCTTTGCCTTCCACTTTATTCTCCCCTTCATAGCATCAGCACTAG	130
odo.ros	CAACCCTAACACGATTCCTCGCCCTCCACTTCGTTCTTCCATTCATGGCATTAGCACTAA	130
pho.fasciata	CAACCCTAACACGATTTTTCGCTTTCCACTTTATCCTACCATTTGTAGTATCAGCACTAG	130
pho.gro	CAACCCTAACACGATTTTTCGCCTTCCACTTCATCTTACCATTCGTAGTATTAGCACTAG	130
pho.vit	CAACCTTAACACGATTCTTCGCCTTCCACTTCATCCTGCCATTCGTAGTATCAGCCCTAG	130
cys.cri	CAACTCTAACACGGTTTTTCGCCTTCCACTTCATCCTACCATTCGTCGTATCAGCACTAG	130
hyd.lep	CAACCCTAACACGATTCTTCGCCTTCCACTTTATCCTTCCCTTCGTAGTATCAGCACTAG	130
lep.wed	CAACCCTAACACGATTCTTCGCCTTCCACTTTATCCTTCCCTTCGTAGTATCAGCACTAG	130
mir.leo	CAACCCTAACACGATTCTTCGCCCTCCACTTTATCCTACCATTCGTAGCACTAGCACTAG	130
eri.bar	CAACCCTAACACGATTCTTCGCCTTCCACTTTATCCTACCATTTGTAGTATTAGCATTAG	130
mon.sch	CAACCCTAACACGATTCTTCGCTTTCCATTTTATTATACCCTTCATAGTATTAGCACTAG	130
hela.mal	CGACTCTAACACGATTCTTTGCCTTCCACTTTATCCTTCCGTTCATCATCTTGGCACTAA	130
sel.thi	CAACCCTAACACGATTCTTTGCTTTCCACTTTATCCTTCCGTTCATCATCCTAGCACTAG	130
ail.ful	CAACTCTAACTCGATTCTTCGCCTTCCACTTCATTCTTCCATTTATCATTGCAACACTAG	130
fel	CCACCCTAACACGATTCTTTGGCTTCCACTTCATTCTTCCATTCATTATCTCAGCCTTAG	130
can	CAACCCTAACACGATTCTTTGCATTCCATTTCATCCTCCCTTTCATCATCGCAGCTCTAG	130
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gla.vol	CTACCTTAACCCGATTCTTTGCATTTCACTTCATTCTTCCTTTTATCATTGCCGCTCTAG	130
hyl.pha	CTACCCTAACCCGATTCTTCGCATTCCACTTTGTGCTGCCCTTTATTATTGCAGCACTAG	130
pet.set	CTACCCTAACCCGATTCTTCGCATTCCACTTTGTGCTGCCCTTTATTATTGCGGCACTGG	130
bel.pea	CAACCCTAACACGATTCTTCGCATTCCACTTTATCTTACCATTTATCGTAGCAGCCCTTG	130
pte.mom	CTACCCTAACACGATTCTTTGCATTCCACTTTGTCCTCCCTTCATTATCGCAGCCCTAG	130
gala.demi	CTACCCTTACCCGATTCTTTGCTTTCCACTTTATCCTCCCATTTATCATTACAGCAATAG	130
pero.pot	CTACCCTAACACGATTCTTCGCCTTCCACTTCATCCTCCCCTTTATTATCACAGCACTAG	130
gala.mat	CCACCCTTACTCGATTCTTCGCTTTTCACTTCATCCTACCTTTCATTATTGCAGCCCTAG	130
gala.moh	CTACTCTTACCCGATTTTTCGCTTTTCACTTCATCCTGCCTTTCATCATCGCGGCCCTAG	130
oto.gar	CAACCCTCACCCGGTTTTTTGCTTTCCACTTTATCCTGCCTTTCATCATCGCAGCCCTAG	130
lor.tar	CAACCCTCACACGATTCTTCGCCTTTCACTTCATCCTTCCATTCATCATCACAGCATTAA	130
nyc.cou	CAACCCTCACACGATTCTTCGCCTTCCACTTTATCCTCCCCTTCATCGTCGCTGCTTTAG	130
mus	CCACACTCACACGATTCTTCGCTTTCGACTTCATCTTACCATTTATTATCGCGGCCCTAG	130
gorr	CCACCTTGACCCGATTCTTCGCTTTCCACTTTATCCTACCCTTCATCATCACAGCCCTAA	130
homo	CTACCCTTACACGATTCTTTACCTTTCACTTCATCTTGCCCTTCATTATTGCAGCCCTAG	130
dug.dug	CCACCCTCACACGATTCTTTAGCCTTACACTTCATCTTACCCTTCATCGTAACCGCCCTAG	130
ele.max	CCACCCTCACCCGATTCTTCGCCTTCGATTTCATCCTTCCATTTACTATAGTTGCACTAG	130
afr.con	CAACCTTAAACCGATTCTTCGCCTTAGACTTTCTTCTCCCCTTTTTTGTAATTGCGGGAATTA	130
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tra.bly	CAACCCTCACCCGATTCTTCGCCTTAGACTTTCTTCTTCCATTTTGTAATTGCAGGAATTA	130
tra.gat	CAACCCTCACTCGATTCTTCGCCTTAGACTTTCTTCTTCCATTTTGTAATTGCAGGAATTA	130
tra.rob	CAACCCTCATCCGATTCTTCGCCTTAGACTTTCTTCTTCCATTTTGTAATTGCAGGAATTA	130
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arg.arg	CAACCTTTATCCGATTCTTTCTCCTTAGATTTCTTCTTTTATTTTGTAATTGCAGGAATTA	

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cat.wal        CAACTCTCACCCGATTCTTCGCCCTGCACTTCCTCCTTCCCTTCGTAATTGCAGGAATCA 180
cro.cro        CAACCCTCACCCGATTCTTCGCCCTACACTTCCTCCTCCCCTTCGTAATTGCAGGAATTA 180
sym.ree        CAACCCTCACCCGATTCTTCGCCCTTCACTTTCTCCTACCCTTCGTAATCACAGGAATCA 180
bam.tho        CAACTCTCACCCGATTCTTCGCCTTACACTTCCTACTCCCCTTCGTAATCGCAGGAATTA 180
fra.fra        CAACCCTCACCCGATTCTTCGCCCTACACTTCCTTCTCCCCTTCGTAATTGCAGGAATCA 180
ith.cru        CAACCCTCACCCGATTCTTCGCCCTACACTTTCTCCTCCCCTTCGCAATCGCAGGAATTA 180
ant.par        CCACATTAACTCGATTCTTCACTTTACACTTCCTCCTTCCATTCATAATTATGGCCTCA 180
ant.vir        CCACATTAACTCGATTCTTCACGTTACACTTCCTCCTTCCATTCATAATTATGGCCTCA 180
gru.ant.ant    CCACATTAACTCGATTCTTCACTTTACACTTCCTCCTTCCATTCATAATCATAGGCCTCA 180
gru.ant.gil    CCACATTAACTCGATTCTTCACTTTACACTTCCTCCTTCCATTCATAATCATAGGCCTCA 180
gru.ant.sha    CCACATTAACTCGATTCTTCACTTTACACTTCCTCCTTCCCTTCATAATCATAGGCCTCA 180
gru.leu        CCACATTAACTCGATTCTTCACTTTACACTTCCTCCTTCCATTCATAATCATAGGCCTCA 180
gru.can.pra    CCACATTAACCCGATTCTTCACTTTACACTTCCTCCTCCCATTCATAATTATAGGCCTCA 180
gru.can.row    CCACATTAACCCGATTCTTCACTTTACACTTCCTCCTCCCATTCATAATTATAGGCCTCA 180
gru.can.tab    CCACATTAACCCGATTCTTCACTTTACACTTCCTCCTCCCATTCATAATTATAGGCCTCA 180
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gru.ame        CCACATTAACCCGATTCTTCACTTTACACTTCCTCCTCCCATTCATAATCATAGGCCTCA 180
gru.gru        CCACATTAACCCGATTCTTCACCTTACACTTCCTCCTCCCATTCATAATCATAGGCCTCA 180
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gru.nig        CCACATTAACTCGATTCTTCACCTTACACTTCCTCCTCCCATTCATAATCATAGGCCTCA 180
gru.jap        CCACATTAACTCGATTCTTTACCTTACACTTCCTCCTCCCATTCATAATCATAGGCCTCA 180
cic.boy        CAACACTAACCCGATTCTTCGCCCTACACTTTCTTCTCCCCTTCGCAATCGCAGGCCTCA 180
rhe.ame        CTACCCTAACCCGATTCTTCGCCCTGCACTTCCTTCTCCCCTTCCTAATCGCAGGCATTA 180
ant.alb        CAACCCTGACACGATTCTTCGCCCTACACTTTCTCCTCCCGTTCATAATCGCAGGCCTAG 180
fal.fam        CAACACTGACCCGATTCTTCGCCCTACACTTCCTCCTACCATTCCTAATCGCAGGGCTCA 180
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smi.sha        CCACCCTTACCCGATTCTTCTCCCTTCACTTCCTCCTCCCATTTATCATCGCAAGCCTGA 180
vid.cha        CAACACTCACCCGATTCTTCGCCCTACACTTCCTTCTACCCTTCGTCATTGCAGGACTCA 180
chry.pic       CAACCTTAACCCGATTTTTTACCCTTCACTTCCTTCTACCATTTACAATCATAGGTCTAA 180
emy.orb.kur    CAACCCTAACCCGATTCTTCACTTTCCATTTCTTACTGCCATTTACCATTATAGGCCTAA 180
che.mud        CAACCCTAACCCGATTCTTCACCTTCCACTTCCTATTACCATTTGCCATTACCGGCCTTA 180
eum.egr        CAACCCTCACCCGATTTTTCACATTCCACTTCCTTCTGCCATTCGCTATTATAGGGGCCT 180
               *  *  *  *  ** **  *      * ** **        ** **

aep.mel        CCATAGTCCACCTACTCTTTCTTCACGAAACAGGATCTAACAACCCTACAGGAATCTTAT 240
cre.cre        CCATAGTACACCTACTCTTTCTCCACGAAACAGGGTCCAATAACCCCACAGGAATCTCAT 240
add.nas        CCATAGTCCATCTACTCTTTCTCCACGAAACAGGCTCCAACAACCCTACAGGAATCTCCT 240
ory.dam        CCATAGTCCACCTACTCTTTCTCCACGAAACAGGCTCCAACAACCCTACAGGAATCACCT 240
hip.equ        CCATAGTACACCTACTCTTTCTCCATGAGACAGGCTCCAACAACCCCACAGGAATTTGAT 240
alc.bus        CCATAGTTCACCTCTTATTCCTCCACGAAACAGGATCTAACAACCCCACAGGAATCTCAT 240
sig.lic        CCATAGTTCACCTCTTATTCCTCCACGAAACAGGATCTAACAACCCCACAGGAATCTCGT 240
bea.hun        CCATAGTCCACCTCTTATTTCTCCACGAAACAGGATTTAACAACCCCACAGGAATCTCGT 240
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con.tau        CTATAGTCCATCTCCTATTCCTCCACGAAACAGGATCTAACAATCCCACAGGAATTTCAT 240
amm.ler        CCATAGTCCACTTACTTTTCCTCCATGAAACGGGATTCAACAACCCCACAGGAATTTCAT 240
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nem.gor        CTATAGTCCACCTACTTTTCCTCCATGAGATAGGATTCAACAATTCCACAGGTATCCCAT 240
bud.tax.tax    CCATAGTCCATTTACTTTTCCTCCACGAAACAGGATTCAACAATTCCACAGGAATTCCGT 240
pan.hod        TTATAGTCCACCTACTCTTCCTCCACGAAACAGGATTTAACAATTCCACAGGAATTCCAT 240
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ore.ame	CCATAGTCCACTTACTTTTCCTCCACGAAACAGGATCTAATAACCCAACAGGAATTTTAT	240
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bos.gru	CCATAGTCCACCTACTATTCCTCCACGAAACAGGCTCCAACAATCCAACAGGAATCTCCT	240
bos.tra	CAATAATCCATCTACTCTTCCTCCATGAAACAGGGTCTAACAATCCAACAGGAATTTCAT	240
bub.min	CAATAGTCCACCTATTATTTCTCCACGAAACAGGATCCAACAACCCAACAGGAATCTCAT	240
buba.bub	CAATAGTCCACCTATTATTTCTCCACGAAACAGGATCCAACAACCCAACAGGAATCTCAT	240
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tra.eur	CCATGGTACACCTACTATTCCTCCACGAAACAGGATCCAACAACCCAACAGGRATCTCAT	240
kob.ell	CCATAGTCCATCTTCTGTTTCTCCATGAAACAGGATCCAATAATCCCACAGGAATCTCAT	240
kob.meg	CTATAGTTCACCTACTATTCCTTCATGAAACAGGATCTAACAACCCTACAGGGATTTCAT	240
red.aru	CTATAGTACACCTACTATTCCTCCACGAAACAGGATCCAACAACCCTACAGGAATCTCAT	240
red.ful	CTATAGTCCACCTACTATTCCTCCATGAAACAGGATCCAACAACCCCACAGGGGTTTCAT	240
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pel.cap	CCATAGTACACTTGCTTTTTCTTCATGAAACAGGATCTAATAACCCCACGGGAATTCCAT	240
gaz.dam	CCATAGTTCATCTATTATTTCTTCACGAAACAGGATCCAACAACCCCACAGGAATTTCAT	240
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sai.tat	CTATAGTCCACCTACTTTTTCTTCACGAAACAGGATCTAACAACCCCACAGGAATCCCAT	240
mad.kir	CCATGGTTCACCTCCTCTTTCTCCATGAAACGGGATCCAACAGCCCCACAGGCATTTCAT	240
rap.mel	CTATAGTTCACCTACTTTTCCTCCACGAAACTGGATCCAACAACCCCACAGGAAGTTTAT	240
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ant.ame	CCATAGTACACTTACTATTCCTCCACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
hyd.ine	CCATAGTGCACTTACTTTTTCTCCACGAAACAGGATCCAATAACCCAACAGGAATTCCAT	240
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cer.dam	CTATAGTACATTTACTCTTTCTTCACGAGACAGGATCCAATAACCCAACAGGAATTCCAT	240
ran.tar	CTATAGTCCATTTGCTTTTCCTTCACGAAACAGGGTCTAACAATCCAACAGGAATCACAT	240
mos.fus	CTATGGTTCACCTACTCTTTCTCCACGAAACAGGATCCAACAACCCAACAGGAATCACAT	240
mos.leu	CTATGGTTCACCTACTCTTTCTCCACGAAACAGGATCCAACAACCCAACAGGAATCACAT	240
mos.chr	CTATGGTTCACCTACTCTTTCTCCACGAAACAGGATCCAACAACCCAACAGGAATCATAT	240
mos.ber	CTATGGTTCACCTACTCTTTCTCCACGAAACAGGATCCAACAACCCAACAGGAATCACAT	240
mos.mos	CCATGGTTCATCTACTCTTTCTCCATGAAACAGGATCCAATAACCCAACAGGAATCACAT	240
tra.jav	TCCTAGTCCACCTTTTATTTCTCCACGAAACAGGATCTAATAACCCCACAGGAATCCCCT	240
trag.nap	CCCTAGTCCATCTTTTATTTCTCCACGAGACAGGATCAAATAACCCCACAGGAATCCCCT	240
bala.atu	CAATTGTCCACCTCATTTTCCTCCACGAAACAGGATCCAATAACCCCACAGGTATCCCAT	240
bala.bon	CAATTGTCCACCTCATTTTCCTCCGCGAAACAGGATCCAATAACCCCACAGGTATTCCAT	240
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esch.rob	CAATTGTCCACCTCATTTTCCTCCACGAAACGGGATCCAACAACCCCACAGGCATTCCAT	240
bala.mus	CAATCGTCCACCTCATCTTCCTTCACGAAACAGGATCCAACAACCCCACAGGTATCCCAT	240
mega.nov	CAATCGTCCACCTCATTTTCCTCCACGAAACAGGATCCAACAACCCCACAGGCATCCCAT	240
bala.phy	CAATTGTCCACCTTATTTTCTTCACGAAACAGGATCCAACAACCCCACAGGCATCCCAT	240
cip.mar	CAGCTGTTCATCTTCTTTTCTTCACGAAACAGGATCCAACAACCCCACAGGCATCCCAT	240
ceph.com	CAGCCGTCCACCTACTTATTCCTACACGAAACAGGATCCAACAACTTTACAGGAATCCCAT	

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ceph.eut	CAGCCGTCCACCTACTATTCCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
lage.obl	CAGCCGTCCACCTACTATTCCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
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ceph.hec	CAGCCGTCCACCTACTATTCCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
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lage.cru	CAGCCGTCCACCTGCTATTCCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
lage.obs	CAGCCGTCCACCTACTATTCCTACACGAAACAGAATCCAACAACCCCACAGGAATCCCAT	240
lisso.bor	CAGCTGTTCACCTACTATTCCTACACGAAACAGGATCCAACAACCCCACAGGAATTCCAT	240
lisso.per	CAGCTGTTCACCTACTGTTCCTACACGAGACAGGATCCAATAACCCCACAGGAATTCCAT	240
glo.mac	TAGCTGTCCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCCATAGGAATCCCAT	240
glo.mel	TAGCTGTCCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCCATAGGAATCCCAT	240
fere.att	TAGCTGTTCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
pepo.ele	TAGCTGTCCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCTACAGGAATCCCAT	240
gram.gri	TAGCTGTTCACCTGCTATTCCTACACGAGACAGGATCCAATAACCCCACAGGAATCCCAT	240
pse.cra	CAGCTACCCACCTACTATTCCTACACGAGACTGGATCCAATAACCCCACAGGAATCCCAT	240
lage.acu	CAGCTGTTCACCTGCTGTTCCTACACGAGACAGGATCCAATAACCCTACAGGAATCCCAT	240
orci.bre	CAGCTGTTCACCTACTGTTCCTACACGAGACAGGATCCAATAACCCCACAGGAATCCCAT	240
orca.bre	TAACTGTTCACCTACTATTCCTACACGAAACAGGATCCAACAATCCTACAGGAATCCCAT	240
del.cap	CAGCCGTTCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
del.tro	CAGCCGTTCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
del.del	CAGCCGTTCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
sten.cly	CAGCCGTTCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCCACAGGAATTCCAT	240
sten.coe	CAGCCGTTCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCAACAGGAATTCCAT	240
tur.adu	CAGCCGTTCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
sten.fro	CAGCCGTTCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCCACAGGAATCCCAT	240
saus.chi	CAGCCGTTCACCTACTATTCCTACACGAAACAGGATCCAATAACCCTACAGGAATTCCAT	240
sten.lon	TAGCCGTTCACCTGCTATTCCTACACGAAACAGGATCCAATAACCCTACAGGAATCCCAT	240
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lage.alb	CAGCCGTTCACCTACTATTCCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
sten.bre	TAGCTGTTCACCTACTATTTTTACACGAGACAGGATCCAACAACCCCACAGGAATCCCAT	240
sota.flu	CAACTGTCCACCTACTATTCCTACACGAGACAGGATCCAACAATCCCACAGGAATCCCAT	240
del.leu	CAGCCGTTCACCTGCTATTCCTACACGAAACAGGATCCAATAATCCCACAGGAATCCCAT	240
mono.mon	TAGCCGTCCATTTATTATTCCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
plat.gan	TGGCCGTCCACTTATTATTCCTACACGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
plat.min	CAATTATCCACCTACTATTCCTACACGAAACAGGCTCAAACAACCCCACAGGAATTCCAT	240
kogi.bre	CAGTTATCCACCTACTATTCCTACACGAAACAGGCTCAAACAACCCCACAGGAATTCCAT	240
kogi.sim	CAATGGTCCACCTCTTATTTCTCCACGAAACAGGATCCAACAACCCCATAGGAATCCCAT	240
phys.cat	CAATAATCCACCTCCTATTTCTCCACGAAACAGGATCCAACAACCCCCTAGGAATTCCTT	240
lipo.vex	CAATAGTACATCTCCTATTTCTCCATGAAACAGGATCCAACAACCCCACAGGAATTCCCT	240
phoc.sin	CAACCGTCCACTTACTATTTCTCCATGAAACAGGATCCAACAACCCAATAGGAATTCCAT	240
bera.bai	CAACCGTCCACTTACTATTTCTCCATGAAACAGGCTCCAACAATCCCACAGGAATCCCGT	240
ziph.car	TAATCGTCCATCTACTATTCCTCCATGAAACAGGATCCAACAACCCCACAGGAATCCCAT	240
meso.eur	CAGCCGTCCACTTACTATTCCTCCACGAAACAGGATCTAATAACCCCACAGGAATCCCAT	240
meso.bid	CAGCCGTCCACTTACTATTTCTCCACGAAACAGGATCCAATAACCCTACAGGAATCCCAT	240
meso.den	CAATCGTCCACTTACTATTTCTCCATGAAACAGGATCCAATAACCCTACAGGAATTCCAT	240
hype.amp	CAATCGTCCACCTACTATTTCTCCATGAAACAGGATCTAACAACCCTACAGGAATCCCAT	240
meso.per	CAATGGTCCACCTACTATTCCTCCATGAAACAGGATCTAATAACCCTACAGGAATCCCAT	240
pont.bla	CAATCGTCCACCTACTATTCCTCCATGAAACAGGATCCAACAATCCCACAGGAATTCCAT	240
hex.lib	CAATCGTCCACCTACTATTCCTCCATGAAACAGGATCTAATAATCCCATAGGAATCTCTT	240
hipp.amp	CAATTGTCCATTTACTATTTCTACACGAAACAGGATCTAATAATCCCATAGGAATCTCAT	240
dic.sum	TTATAGTCCACCTGCTATTCCTACACGAAACTGGATCCAACAACCCAACAGGAATCCCCT	240
rhin.son	CCGCCGTCCACCTACTGTTTCTCCACGAAACAGGGTCCAACAACCCAACAGGAATCCCCT	240
cera	CCATCGTCCATCTACTATTCCTCCATGAAACAGGATCCAACAACCCATCAGGAATCCCAT	240
equu	CAATTACCCACCTGCTATTCCTACATGAAACAGGATCCAACAACCCATCAGGAATTCCAT	240
baby.bab	CGATCACCCACTTACTATTCCTACACGAAACAGGATCCAATAACCCATCAGGAATCCCAT	240
phac.afr	CAATCACCCACCTACTATTCCTTCACGAAACAGGATCCAATAACCCATCAGGAATCCCAT	240
sus.bar	TAATCGTCCATCTACTATTCCTCCACGAAACAGGATCCAACAACCCCTCAGGAATCCCAT	240
sus.scr.ewb1	CAACCGTACATCTATTATTCCTTCACGAAACTGGATCCAATAACCCTACTGGAATTTCAT	240
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vic.vic	CGGGAGTACATCTACTATTTTTACACGAAACAGGCTCCAACAACCCAACAGGAATTTCTT	240
cam.bac	TAGCCGTACACCTATTATTCCTACACGAAACAGGCTCTAATAACCCGACAGGAATCTCCT	240
arc.for	TAATAGTACATCTGCTATTCCTACATGAAACAGGATCCAATAACCCATCAGGAGTCTCCT	240
arc.gaz	TAATAGTGCACCTACTATTCCTACACGAAACAGGATCCAACAACCCATCAGGAGTCTCCT	240
eum.jub	TAATAGTACACCTATTATTCCTACACGAAACTGGATCCAACAATCCATCAGGAATCTCCT	240
zal.cal	TAATAGTACACCTATTATTCCTACACGAAACTGGGTCCAACAACCCATCAGGAATCTCCT	240
odo.ros	CAGCAGTACACCTACTATTTCTCCACGAAACAGGATCTAACAACCCTTCGGGAATCCTAT	240
pho.fasciata	CGGCAGTTCACCTACTATTCCTACACGAAACAGGATCCAACAACCCCTCCGGAATCGTAT	240
pho.gro	CGGCAGTTCATCTACTATTCTTACACGAAACAGGATCCAACAACCCCACCGGAATCGTAT	240
pho.vit	CAGCAGTCCACCTACTATTCCTACACGAAACAGGATCAAACAACCCCTCCGGAATCATAT	240
cys.cri	CAACAGTCCACCTACTATTCCTACACGAAACAGGATCTAATAATCCCTCCGGAATCACAT	240
hyd.lep	CAGCAGTACATCTACTATTCTTACACGAAACAGGATCCAATAACCCCTCCGGAATTCCAT	240
lep.wed	CAGCAGTACATCTACTATTCTTACACGAGACAGGATCCAACAACCCCTCCGGAATTCCAT	240
mir.leo	CAGCAGTACATCTACTATTCCTACACGAAACAGGATCCAACAACCCCTCTGGAATCCCAT	240
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mon.sch	CAGCAGTCCATTTATTATTTCTACACGAAACAGGATCCAACAATCCCTCCGGAATTCCAT	240
hela.mal	CAGCGGTCCACCTATTATTCCTACACGAAACAGGGTCCAACAATCCCTCTGGAATCCCAT	240
sel.thi	CAGCAGTTCATCTATTGTTCCTACACGAAACAGGATCCAACAACCCTTCTGGAATCCCAT	240
ail.ful	CAACTATCCATCTCTTATTCCTACATGAAACAGGATCTAATAACCCCTCAGGCATCCCAT	240
fel	CAGGAGTACACCTCTTATTCCTTCATGAAACAGGATCTAACAACCCCTCAGGAATTACAT	240
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tal	CTGGAGTTCACCTGTTATTTCTTCACGAAACAGGATCAAACAACCCATCAGGACTCTCAT	240
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gla.vol	CCATAATCCATCTACTCTTTCTACACGAAACAGGATCCAATAACCCATCAGGACTAATCT	240
hyl.pha	CTATAATTCACCTTCTCTTTCTACACGAAACAGGATCAAATAACCCATCAGGCCTAATTT	240
pet.set	CTATAATCCACCTTCTCTTTCTACACGAAACAGGGTCAAATAATCCATCAGGTCTAATTT	240
bel.pea	CAATAGTCCACCTTCTTTTCCTCCACGAAATTGGGTCAAATAATCCCCCCGGATTAATTT	240
pte.mom	CAATAGTTCACCTACTTTTCCTTCATGAAACAGGGTCCAACAACCCATCTGGACTTACCT	240
gala.demi	TCATAATCCACCTCCTATTCCTTCACGAAACAGGATCAAACAACCCCTCAGGACTTCCAT	240
pero.pot	CCACAACTCACCTCTTATTTCTTCACGAAACAGGATCAAATAACCCAGCAGGAATTCCAT	240
gala.mat	CCATAATTCACCTTCTTTTCCTACATGAAACAGGATCAAACAACCCTTCAGGAATCTCAT	240
gala.moh	CCATAATTCATCTTCTTTTTTTACATGAAACAGGGTCAAATAACCCTTCGGGAATCTCAT	240
oto.gar	TCATAATCCACCTCCTTTTCCTCCACGAATCAGGATCAAACAACCCTTCAGGAATCCCAT	240
lor.tar	CTGCAATTCACCTACTTTTCCTACACGAATCAGGATCAAATAACCCATCCGGAATAACAT	240
nyc.cou	TTGTGATTCACCTCATCTTTCTACATGAAACAGGCTCAAATAATCCATCAGGAATCTCAT	240
mus	CAATCGTTCACCTCCTCTTCCTCCACGAAACAGGATCAAACAACCCAACAGGATTAAACT	240
gorr	CAACCCTCCATCTCCTATTTCTACACGAAACAGGATCAAACAACCCTCTAGGCATCCCCT	240
homo	CAACACTCCACCTCCTATTCTTGCACGAAACGGGATCAAACAACCCCCTAGGAATCACCT	240
dug.dug	TAATAGTCCACTTACTATTCCTCCACGAAACAGGCTCCAACAACCCCACGGGACTGATCT	240
ele.max	CAGGAGTGCACCTAACCTTTCTTCACGAAACAGGCTCAAACAACCCACTAGGTCTCACTT	240
afr.con	CAATTATCCACCTCACATTCCTTCATGAATCAGGCTCAAACAACCCACTGGGCATCTCAT	240
pavo.mut	CAATTATCCACCTCACATTCCTCCATGAATCAGGCTCAAATAATCCACTAGGCATCTCAT	240
tra.bly	CCATCATGCACCTCATCTTCTTACATGAATCAGGCTCTAATAACCCACTGGGCATCTCAT	240
tra.sat	CTATCATACACCTCATCTTCTTACATGAATCAGGCTCTAATAACCCACTGGGCATCTCAT	240
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tra.tem	CCATCATCCACCTCATCTTCCTACATGAATCAGGCTCAAACAACCCTCTAGGCATCTCAT	240
arg.arg	CCATCATCCACCTCACATTCCTACACGAATCAGGCTCAAACAACCCACTAGGCATCTCAT	240
cat.wal	CCATCACCCATCTCATATTCCTACATGAATCAGGCTCAAATAACCCCCTAGGCATCTCAT	240
cro.cro	CTGTCACCCACCTCATATTCCTACACGAATCAGGCTCAAACAACCCACTAGGCATTTCAT	240
sym.ree	CCATCACACATCTTATGTTCCTACACGAATCAGGCTCAAACAACCCCCTAGGCATCTCAT	240
bam.tho	CCATTATCCACCTCACATTCTTACACGAATCAGGATCAAACAACCCCCTAGGCATCTCAT	240
fra.fra	CTATCATCCACCTCACATTTCTGCACGAATCAGGCTCAAACAACCCCCTAGGCATCTCAT	240
ith.cru	CTGTCATCCACCTTACACTCCTCCACGAATCAGGTTCAAATAACCCACTAGGCATCTCAT	240
ant.par	CCCTAATCCACCTCACCTTTCTTCACGAGTTCGGCTCAAATAACCCCCTAGGCATTGTAT	240
ant.vir	CCCTAATCCACCTCACCTTTCTTCACGAATTCGGCTCAAACAACCCCCTAGGCATCGTAT	240
gri.ant ant	CCCTAATCCACCTCACCTTTCTTCACGAATTCGGCTCAAACAACCCCCTAGGCATCGTAT	240

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gru.ant.gil     CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT 240
gru.ant.sha     CCCTAATCCACCTCACCTTCCTTCACGAATCCGGTTCAAACAACCCCCTAGGCATCGTAT 240
gru.leu         CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT 240
gru.can.pra     CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCCTAGGCATTGTAT 240
gru.can.row     CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAATCCCCTAGGCATTGTAT 240
gru.can.tab     CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCCTAGGCATTGTAT 240
gru.can.can     CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCCTAGGCATTGTAT 240
gru.ame         CCCTAATCCACCTCACCTTCCTCCACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT 240
gru.gru         CCCTAATCCACCTCACCTTCCTTCACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT 240
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gru.nig         CCCTAATCCACCTCACCTTCCTCCACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT 240
gru.jap         CCCTAATCCATCTCACTTTCCTCCACGAATCCGGCTCAAACAACCCCCTAGGCATCGTAT 240
cic.boy         CCCTAATCCACCTCACCTTCCTTCACGAGTCCGGCTCAAACAACCCCCTAGGCATCATCT 240
rhe.ame         CTCTTATCCACCTCACCTTCCTACACGAAACCGGGTCCAACAACCCCTTAGGAATCGTAT 240
ant.alb         TCCTAATTCACCTGGCATTCCTCCACGAATCAGGCTCAAACAACCCACTAGGCATCACAT 240
fal.fam         CCTTAATCCACCTCACCTTCCTACATGAATCAGGTTCAAACAACCCCCTAGGAATCACAT 240
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fal.per         CCCTAATCCACCTCACCTTCCTACATGAATCAGGCTCAAATAACCCCCTAGGAATCACAT 240
fal.spa         CCTTAATCCACCTCACCTTCCTACATGAATCAGGTTCCAACAACCCCCTAGGAGTCACAT 240
ayt.ame         CCCTAGTCCACCTAACTTTCCTGCACGAGTCAGGCTCAAACAACCCCCTAGGCATTGTAT 240
smi.sha         CACTCATCCATCTCACCTTCCTCCATGAAACAGGTTCAAACAACCCTCTAGGTATCTCAT 240
vid.cha         CTCTAGTCCACCTCACATTCCTACACGAAACAGGATCAAACAATCCAATAGGAATTCCAT 240
chry.pic        CAATAGTACACCTACTTTTTCTACATGAAACTGGATCAAACAACCCAACAGGATTAAACT 240
emy.orb.kur     CAATAGTACACCTACTCTTCCTACACGAAACCGGATCAAACAATCCAACAGGATTAAACT 240
che.mud         CAGCAGTACATCTATTATTCCTGCACGAAACAGGATCAAACAACCCAACAGGATTAAATT 240
eum.egr         CAATAATTCACCTACTATTTCTTCACGAAACAGGATCAAATAACCCAACCGGACTAAATT 240
                        **  *     *  * *  **    *  ** ** *  **    **       *

aep.mel         CAGATTCAGATAAAATTCCATTCCACCCTTACTATACTATTRAAGACATCCTAGGAATCC 300
ore.ore         CAGACACAGACAAAATCCCATTTCATCCTTATTACACAATCAAAGATATCCTAGGCGCCC 300
add.nas         CAGACACAGACAAAATCCCATTCCACCCTTACTATACCATTAAAGACATCTTAGGCGCCC 300
ory.dam         CAGACACAGACAAAATTCCGTTCCACCCTTATTATACCATTAAAGATATCTTAGGCGCCC 300
hip.equ         CAGACTCCGATAAAACCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGCGCCC 300
alc.bus         CAGACGCAGATAAAATCCCATTCCACCCCTACTATACAATCAAGGACATTCTAGGCGCCC 300
sig.lic         CAGACGCAGATAAAATCCCATTCCACCCCTACTATACAATCAAGGACATTCTAGGCGCCC 300
bea.hun         CAGATGCAGATAAAATTCCATTCCACCCCTACTACACCATCAAAGACATCCTAGGCGCCC 300
dam.lun         CAGATGCGGACAAAATCCCGTTTCACCCCTACTACACTATCAAAGACGCCCTAGGGGCCC 300
con.tau         CCGACACCGATAAAATCCCATTCCCCCCCTATTACACCATCAAAGACATCCTAGGCGCTC 300
amm.ler         CAGACGCAGACAAAATCCCATTCCACCCTTACTACACCATCAAAGATATTCTAGGCGCCA 300
pse.nay         CAGACACAGACAAAATCCCATTCCACCCTTACTACACCATTAAAGATATTCTAGGCGCTG 300
cap.ibe         CAGACACAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGATATCTTAGGCGCCA 300
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rup.pyr         CAGATGCGGATRAAATCCCATTTCACCCCTACTATACCATTAAAGACATTCTAGGCGCCA 300
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nem.cau         CAGACATAGACAAAATCCCATTTCACCCTTATTATACAATCAAAGATATTCTAGGCGCTA 300
bud.tax.tax     CAGATGCAGATAAAATTCCATTTCACCCTTATTACACCATTAAAGATATCCTAGGAGTCA 300
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ovi.amm         CGGACACAGATAAAATTCCCTTCCACCCTTACTACACCATTAAAGACATCCTAGGTGCCA 300
ovi.vig         CGGACACAGACAAAATCCCCTTCNRRRRRRRRRRRRRRNATTAAAGACATTCTGGGTGCCA 300
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ovi.mos         CAGACACGGACAAAATCCCATTCCACCCCTACTATACAATCAAAGACATTCTAGGCGCCA 300
ore.ame         CAGACGCAGACAAAATTCCATTTCACCCTTACTATACTATTAAAGATATCCTAGGCGCCA 300
cep.dor         CGGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATCCTAGGCGCCC 300
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bis.bon         CAGACACAGACAAAATTCCATTCCACCCTTACTATACCATTAAAGACATCCTAGGAGCCT 300
bos.gru         CAGACGCAGACAAAATTCCATTTCACCCCTACTATACCATTAAAGACATCTTAGGAGCCT 300
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kob.ell	CAGACATAGATAAAATCCCATTCCACCCCTACTACACCATCAAAGACATTCTAGGCGCCC 300
kob.meg	CAGACACAGACAAAATCCCATTCCACCCATATTATACCATCAAAGATATTCTAGGTGCCC 300
red.aru	CAGATGTAGACAAAATCCCATTTCATCCATACTATACTATCAAGGACGTCCTAGGCGCCC 300
red.ful	CAGAYATGGACAAAATCCCATTCCACCCNTACTACACCATCAAAGAYATTCTAGGTGCCC 300
neo.mos	CAGACGCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGCGCCA 300
pel.cap	CCGACATAGACAAAATTCCATTCCACCCATACTACACCATTAAAGATATTCTAGGCGCCT 300
gaz.dam	CAGATGCAGACAAAATTCCGTTCCACCCCTACTACACCATCAAAGACATTCTAGGAGCAC 300
our.our	CAGATGCAGACAAGGTCCCATTCCACCCCTACTACACCATTAAAGACATCCTAGGCGCCT 300
ant.cer	CAGACGCAGACAAAATTCCATTCCACCCCTACTACACTATCAAAGATATCCTAGGAGCTC 300
sai.tat	CAGATTCAGACAAAATCCCATTCCACCCCTACTACACCATTAAAGACATTCTAGGCGCCC 300
mad.kir	CAGACGCAGACGGAATCCCATTCCGCCCCTACTACACTATTAAAGACATCCTAGGCGCCC 300
rap.mel	CAGATATAGACAAAATCCCATTTCACCCCTACTACACCATTAAAGACATTTTAGGAGCCC 300
gaz.gaz	CAGACGCAGACAAAATCCCATTTCACCCCTACTACACCATCAAGGACATTCTAGGAGCAC 300
ant.ame	CAGACGCAGACAAAATCCCATTCCACCCATACTACACCATCAAAGACATTCTAGGAGCAC 300
hyd.ine	CAGATGCAGATAAAATTCCATTTCATCCCTACTACACCATTAAAGATATTCTAGGTGTAC 300
mun.mun	CAGATGTAGACAAAATTCCTTTCCATCCCTACTATACCATTAAAGATATTTTAGGTGCCC 300
alc.alc	CAGACGCAGACAAAATCCCATTTCACCCTTACTACACTATCAAAGATATCTTAGGTGCCC 300
cer.ela.kan	CAGACGCAGACAAAATCCCCTTCCATCCTTACTATACCATTAAAGATATCTTAGGCATCT 300
cer.ela.xan	CAGACGCAGACAAAATCCCCTTCCATCCTTACTATACCATTAAAGATATCTTAGGCATCT 300
cer.ela.can	CAGACGCAGACAAAATCCCCTTCCACCCTTACTATACGATTAAAGATATCTTAGGTATCT 300
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cer.ela.sco	CAGACGCAGACAAAATCCCCTTTCATCCTTATTATACCATTAAAGATATCTTAGGCATCT 300
cer.dam	CAGATGTAGATAAAATTCCCTTTCATCCCTACTACACCATTAAAGATATTTTAGGCATCC 300
ran.tar	CAGACTCAGATAAAATTCCATTCCATCCCTATTATACTATCAAAGACATTCTAGGCATCC 300
mos.fus	CAGATATAGACAAAATCCCATTCCACCCCTACTACACCATCAAAGACATTCTAGGTGTCC 300
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tra.jav	CAGACGCAGACAAAATCCCCTTCCACCCATACTACACTATTAAAGACATTCTAGGGGTTC 300
trag.nap	CAGACGCAGACAAGATCCCCTTCCACCCATACTACACCATCAAAGATGTCCTAGGGGCTC 300
bala.acu	CTGACATAGACAAAATCCCATTCCACCCCTACTACACAATCAAAGACATTCTAGGCGCCC 300
bala.bon	CTGATATAGACAAAATCCCATTCCACCCCTATTACACAATCAAAGACATTCTAGGCGCCC 300
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esch.rob	CCAACATAGACAATATCCCATTCCACCCCTATTACACAATTAAAGACATACTAGGCGCCC 300
bala.mus	CTGACATAGATAAAATTCCATTCCACCCCTACTACACAATTAAAGACATTCTAGGCGCCC 300
mega.nov	CCAACATAGACAAAATCCCATTCCACCCTTACTACACAATCAAAGACACTCTAGGCGCCC 300
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cap.mar	CCAACATAGACAAAATTCCATTCCACCCCTACTACACAATTAAAGACATCCTGGGCGTCC 300
ceph.com	CCAACATAGACATAATCCCATTCCACCCTTATTACACAATTAAAGACATCCTAGGCGCTT 300
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lisso.bor	CCAACATAGACATAATCCCATTCCACCCTTATTACACAATTAAAGACATCCTGGGCGCTT 300
lisso.per	CCAACATAGACATAATCCCATTCCACCCTTATTACACAATTAAAGACATCCTGGGCGCTT

glo.mac	CCAACATAGACATAATTCCATTCCACCCCTATTATACAATTAAAGACATCCTAGGCGCCC	300
glo.mel	CCAACATAGACATAATTCCATTCCACCCCTATTATACAATTAAAGATATCCTAGGCGCCC	300
fere.att	CCAACATAGACATAATTCCATTCCACCCCTATTATACAACTAAAGATATCCTAGGTGCCC	300
pepo.ele	CCAACATAGACATAATTCCATTCCACCCCTATTATACAATTAAAGACATCCTAGGCGCTC	300
gram.gri	CCAACATAGACATAATTCCATTCCACCCCTATTACACAATTAAAGACATCCTAGGCGCCC	300
pse.cra	CCAACATAGACATAATTCCATTCCACCCTTATTACACAATTAAAGATATCCTAGGCGCCC	300
lage.acu	CTAACATAGATATAATCCCGTTCCACCCTTATTATACAATTAAAGATATCCTAGGCGCTT	300
orci.bre	CCAACATAGATATAATCCCATTCCACCCTTATCACACAATTAAAGATACCCTAGGCGCCC	300
orca.bre	CCAACATAGACATAATCCCATTCCACCCTTATCATACATTTAAAGACATCCTAGGCGCCC	300
del.cap	CCAATATAGACATAATCCCATTCCACCCTTATTATACAATCAAAGATATCCTAGGTGCCT	300
del.tro	CCAACATAGACATAATCCCATTCCACCCTTATTATACAATCAAAGATATCCTAGGTGCCC	300
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sten.cly	CCAATATAGACATAATCCCATTCCACCCTTATTATACAATCAAAGATATCCTAGGTGCCT	300
sten.coe	CCAATATAGACATAATTCCATTCCACCCTTATTATACAATTAAAGATATCCTAGGTGCCT	300
tur.adu	CCAATATAGACATAATCCCATTTCACCCTTATTATACAATCAAAGACATCCTAGGTGCCT	300
sten.fro	CCAATATAGACATAATCCCATTCCACCCTTATTATACAATCAAAGACATCCTAGGCGCCT	300
saus.chi	CCAACATAGACATAATCCCATTTCACCCTTATTATACAATCAAAGACATCCTAGGTGCCT	300
sten.lon	CCAACATAGACATAATCCCATTCCACCCTTATTATACAATCAAAGACATCCTAGGTGGCT	300
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lage.alb	CCAACATAGATATAATTCCATTCCACCCTTATTACACAATCAAAGACATCCTAGGCGCTT	300
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sota.flu	CCAACATAGATATAATTCCATTCCACCCTTATTACACAATCAAAGATATCCTAGGCGCCT	300
del.leu	CCAACATGGATACAATCCCATTCCACCCCTACTACACAATCAAAGACATCCTAGGTGCTT	300
mono.mon	CCAACATAGACATAATCCCCTTCCATCCCTACTACACAATCAAAGACATGCTAGGCGCTT	300
plat.gan	CCGACACTGACAAAATCCCTTTCCACCCCTACTACACAATCAAAGACACCCTAGGCGCCC	300
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kogi.bre	CCGACATAGACAAAATCCCATTCCACCCCTACTACACAATCAAGGACATCTTAGGCGCCC	300
kogi.sim	CTGATATAGACAAAATCCCATTCCACCCCTACTACACAATCAAAGATATCCTAGGCGCCC	300
phys.cat	CCAACATAGACAAAATCCCATTCCACCCCTACCACACAATCAAAGACACCATAGGTGCCC	300
lipo.vex	CTAACATAGACAAAATCCCATTCCACCCCTACCACACAATTAAAGATATCTTAGGCGCCC	300
phoc.sin	CTAACATAGACATAATCCCCTTCCACCCTTACTATACAATCAAAGATATCCTAGGCGCCC	300
bera.bai	CCAATATAGATAAAATTCCATTCCACCCCTACTATACAATCAAAGATATCCTAGGAGCCC	300
ziph.car	CCGATATAGACAAAATCCCATTCCACCCTTATTACACAATCAAAGACATCCTAGGAGCCC	300
meso.eur	CTGATATAGACAAAATCCCATTCCATCCTTACTACACAATCAAAGATATCCTAGGGGCTC	300
meso.bid	CCGACATAGATAAAATTCCATTCCACCCCTACTACACAATTAAAGATATCCTGGGAGCCC	300
meso.den	CTGACATAGATAAAATTCCATTTCACCCTTATTACACAATCAAAGATATTTTAGGAGCCC	300
hype.amp	CTGACATAGACAAAATCCCGTTCCACCCATACTACACAATCAAAGACACTCTAGGGGCCC	300
meso.per	CTGACATAGACAAAATTCCATTTCATCCTTACTATACAATTAAAGATATCTTAGGAGCCC	300
pont.bla	CTAACATAGATGCCATCCCATTTCACCCCTACTACACAATTAAAGATATCCTAGGGGCCC	300
hex.lib	CAAACGCAGACAAAATCCCATTCCACCCCTATTACACAATCAAAGATATCCTGGGCGTAC	300
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dic.sum	CTAACATAGACAAAATCCCATTTCACCCATACTATACAATCAAAGACATCCTAGGAGCCC	300
rhin.son	CTAACACAGACAAAATTCCATTTCACCCTTACTACACAATCAAAGACATCCTAGGAGCCC	300
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equu	CTGACATAGACAAAATCCCATTCCACCCGTACTACACAATTAAAGACATCCTAGGACTTC	300
baby.bab	CAGATATAGACAAAATCCCATTCCACCCCTACTATACCATTAAAGACATTCTAGGAGCCC	300
phac.afr	CAGACATAGACAAAATCCCATTCCACCCATACTACACCATTAAAGATATCCTAGGAGCCT	300
sus.bar	CAGACATACACAAAATTCCATTTCACCCATACTACACTATCAAAGACATTCTAGGAGCCT	300
sus.scr.ewb3	CAGACATAGACAAAATTCCATTTCACCCATACTACACTATTAAAGACATTCTAGGAGCAC	300
lama.gla	CGGATATAGACAAAATCCCCTTCCATCCCTACTATACAATTAAAGACATTCTAGGAGTAC	300
lama.gua	CGGATATAGACAAAATCCCCTTCCATCCCTACTATACAATTAAAGACATTTTAGGAGCAC	300
vic.vic	CAGATATAGACAAAATTCCCTTCCATCCCTACTACACAATTAAAGACATCCTAGGAGCAC	300
cam.bac	CAGACATAGACAAAATCCCATTCCACCCCTACTACACAATTAAAGATATCCTGGGAGCCC	300
art.for	CTGACTCAGACAAAATCCCATTCCACCCATATTATACAATTAAAGATATCCTGGGAGCCC	300
art.gaz	CTGACTCGGACAAAATTCCATTCCACCCATATTATACAATTAAAGATATCCTGGGAACCC	300
eum.jub	CCAACTCAGACAAAATTCCATTCCATCCATATTATACAATTAAAGATATCCTAGGAACCC	300
cal.cal	CTGACTCAGACAAAATTCCATTCCACCCATATTATACAATTAAAGATATCCTAGGAACCC	300
odo.ros	CTGACTCAGACAAAATTCCATTTCACCCCTACTACACAATTAAAGATATCCTAGGCCTTA	300

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pho.fasciata    CCGACTCAGACAAAATCCCATTCCACCCATACTATACAATTAAAGATATCCTAGGAGCCC 300
pho.gro         CCGACTCAGACAAAATCCCGCTCCACCCATATTATACAATTAAAGATATCCTAGGAGCCC 300
pho.vit         CCAACTCAGACAAAATCCCATTCCACCCGTACTATACAATTAAAGATATCCTAGGGGCCC 300
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hyd.lep         CCAACTCAGACAAAATCCCATTTCACCCCTACTACACAATCAAAGACATCCTAGGAGCCC 300
lep.wed         CTGACTCAGACAAAATCCCATTTCACCCCTACTACACAATCAAAGACATCCTAGGAGCCC 300
mir.leo         CCGACTCAGACAAAATCCCATTCCACCCATACTACACAATCAAAGATATCTTAGGAGCCC 300
eri.bar         CCGACTCAGATAAAATTCCATTCCACCCATACTATACAGTCAAGGACATCTTAGGGGCCT 300
mon.sch         CCAACTCAGACAAAATCCCATTCCACCCATACTATACAATTAAAGACATTCTAGGAGCTT 300
hela.mal        CTGACTCAGACAAAATCCCATTTCACCCGTACTATACAATTAAGGACATCCTAGGCGCCC 300
sel.thi         CCAACTCGGACAAAATCCCATTTCACCCATACTATACAATTAAAGACGCCCTAGGCGCCC 300
ail.ful         CCAACTCAGACAAAATTCCATTCCATCCCTATTATACAATTAAAGATATCTTGGGCGCTC 300
fel             CCGATTCAGACAAAATCCCATTCCACCCATACTATACAATCAAAGACATCCTAGGTCTTC 300
can             CAGACTCAGACAAAATTCCATTTCACCCTTACTACACAATCAAGGATATCCTAGGAGCCT 300
tal             CAGATACGGATAAAATTCCATTTCACCCCTATTACACTATTAAAGACATCCTAGGAGCAC 300
gla.sab         CTGACTCAGATAAAATCCCATTCCACCCTTATTTCTCAATTAAAGACACCCTAGGATTCT 300
gla.vol         CTGACTCAGACAAAATCCCATTCCACCCCTACTTCTCAATTAAAGATACCCTAGGATTCT 300
hyl.pha         CCGATTCAGACAAAATCCCATTTCACCCATACTATTCAATTAAAGATCTCCTAGGCGCCC 300
pet.set         CCGATTCAGACAAATTCCCATTTCACCCATACTATTCAATTAAAGATCTCCTAGGGGCCC 300
bel.pea         CTGAATCTGATAAAGTACCATTCCACCCATACTTCACAATCAAAGATATTCTTGGCGCCC 300
pte.mom         CCGAATCCGACAAAATCCCATTCCACCCCTACTTCACAATTAAAGACATTTTAGGAGCAC 300
gala.demi       CAGACTCAGACAAAATCCCCTTTCACCCCTATTACATAATCAAGGATCTCCTAGGACTGA 300
pero.pot        CAGAATCAGACAAAATCCCCTTCCACCCCTACTACACCACCAAAGACTTACTAGGAGCCA 300
gala.mat        CAGACTCCGACAAAATCCCATTCCACCCCTACTACACAATTAAAGACCTACTAGGAGTAA 300
gala.moh        CAGACTCCGACAAAATCCCCTTCCACCCCTACTACACAATTAAAGACCTACTAGGAGCAA 300
oto.gar         CAGACTCTGACAAAATCCCCTTCCACCCCTATTACACAATTAAAGACCTTCTAGGGGCTA 300
lor.tar         CAGACTCTGACAAAATCCCATTTCACCCCTACTACACATTAAAAGATATTCTAGGAGTAA 300
nyc.cou         CAGACTCAGATAAGATTCCATTTCACCCCTACTACTCACTTAAAGACCTCCTAGGAGTGG 300
mus             CAGATGCAGATAAAATTCCATTTCACCCCTACTATACAATCAAAGATATCCTAGGTATCC 300
gorr            CCCACTCTGACAAAATCACCTTCCACCCCTACTACACAATCAAAGACATCCTAGGCCTAT 300
homo            CCCATTCCGATAAAATCACCTTCCACCCTTACTACACAATCAAAGACGCCCTCGGCTTAC 300
dug.dug         CCGACTCAGACAAAATCCCATTCCACCCATATTATTCAGTCAAAGACCTCCTAGGCCTAT 300
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pavo.mut        CCAACTCAGACAAAATTCCGTTCCACCCATACTACTCCCTCAAAGATATCCTAGGCTTAA 300
tra.bly         CTAACTCTGACAAAATCCCATTCCACCCGTACTACTCCCTCAAAGATATCCTGGGTCTAA 300
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tra.cob         CTGACTCTGACAAAATCCCATTCCACCCGTACTACTCCCTCAAAGATATCCTGGGCCTAA 300
tra.tem         CTAACTCTGACAAAATCCCATTCCACCCGTACTACTCCCTCAAAGATATCCTAGGCCTAA 300
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cat.wal         CTAACTCCGACAAAATCCCATTCCACCCATACTACTCCCTCAAAGATATCCTAGGCCTAG 300
cro.cro         CTAATTCCGACAAAATCCCATTCCACCCCTACTACTCCCTCAAAGACATCCTAGGCCTAG 300
sym.ree         CTAACTCTGACAAAATCCCCTTTCACCCATACTACTCTCTCAAAGATATCCTAGGCCTAG 300
bam.tho         CTAACTCCGACAAAATCCCATTCCACCCATACTACTCCTTTAAAGACATTCTCGGCCTAG 300
fra.fra         CTGACTCTGACAAAATCCCATTCCACCCATACTACACCCTCAAAGACATCCTAGGCCTAA 300
ith.cru         CTAACTCTGACAAAATCCCATTTCACCCATACTACTCCCTCAAAGACATCCTAGGCCTAG 300
ant.par         CAAACTGCGATAAAATCCCATTCCACCCCTATTTTTCCTTAAAAGATATCCTAGGATTCA 300
ant.vir         CAAACTGCGATAAAATCCCATTCCACCCCTATTTTTCCTTAAAAGATATCCTAGGATTCA |300
gru.ant.ant     CAAACTGCGATAAAATCCCATTCCACCCCTACTTTTCCTTAAAAGATATCCTAGGATTCA 300
gru.ant.gil     CAAACTGCGATAAAATCCCATTCCACCCCTACTTTTCCTTAAAAGATATCCTAGGATTCA 300
gru.ant.sha     CAAACTGCGATAAAATCCCATTTCACCCCTACTTTTCCTTAAAAGATATCCTAGGATTCA 300
gru.leu         CAAACTGCGATAAAATCCCATTTCACCCCTACTTTTCCTTAAAAGATATCCTAGGGTTCA 300
gru.can.pra     CAAACTGCGATAAAATCCCATTTCATCCCTATTTTTCCTTAAAAGATATCCTAGGGTTCA 300
gru.can.row     CAAACTGCGATAAAATCCCATTTCACTCCTATTTTTTCTTAAAAGATATCCTAGGGTTCA 300
gru.can.tab     CAAACTGCGATAAAATCCCATTTCACCCCTATTTTTCCTTAAAAGATATCCTAGGGTTCA 300
gru.can.can     CAAACTGCGATAAAATCCCATTTCACCCCTATTTTTCCTTAAAAGATATCCTAGGGTTCA 300
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gru.nig        CAAACTGCGATAAAATTCCATTCCACCCCTATTTTTCCTTAAAAGATACCCTAGGATTCA 300
gru.jap        CAAACTGTGATAAAATCCCATTCCACCCCTATTTTTCCTTAAAAGATATCTTAGGATTTA 300
cic.boy        CAAACTGCGACAAAATTCCATTCCACCCCTACTTCTCCCTCAAAGATATCCTAGGCCTTA 300
rhe.ame        CTCACTCTGACAAAATCCCATTCCACCCCTACTTCTCCCTAAAAGATGCCCTAGGACTAG 300
ant.alb        CCAACTGCGACAAAATCCCATTCCACCCATACTTTGCCCTAAAGGACATCCTAGGATTCA 300
fal.fam        CAAACTGCGATAAAATCCCATTCCATCCCTATTACTCTCTCAAAGACCTCCTAGGATTCA 300
fal.ver        CAAACTGCGACAAAATCCCATTCCATCCCTACTACTCTCTAAAAGACCTTTTAGGAGTCA 200
fal.per        CAAATTGCGACAAAATCCCATTCCACCCATACTACTCTCTCAAAGATATCCTAGGATTTA 300
fal.spa        CAAACTGTGACAAAATCCCATTCCACCCCTACTACTCTCTCAAAGACCTCCTAGGTTTTA 300
ayt.ame        CAGACTGCGACAAAATCCCATTTCACCCCTACTTCTCCTTCAAAGACATCCTAGGATTTA 300
smi.sha        CTAACTCCGATAAAATCCCATTCCACCCATACTTCTCCATAAAAGACATTCTAGGCTTTG 300
vid.cha        CAGACTGTGACAAAATTCCATTCCACCCATACTACACCACAAAGGACATCCTAGGCTTCG 300
chry.pic       CAAACACTGACAAAATCCCATTCCACCCTTATTTCTCATATAAAGACCTTTTAGGCGTCA 300
emy.orb.kur    CAAACACCGATAAAATCCCTTTCCATCCCTACTTCTCATACAAAGACCTATTAGGACTCA 300.
che.mud        CAAATACCGACAAAATCCCCTTCCACCCCTACTTCTCCTACAAAGACTTACTAGGACTCA 300
eum.egr        CTAGCACAGATAAGGTGCCATTCCACCCATATTACACATACAAAGACCTTCTTGGTTTCA 300
               *         **        *   *                     * **      * **

aep.mel        TATTAATAATTCTAGTCCTAATACTCCTAGTACTATTCATACCCGACCTACTAGGAGACC 360
ore.ore        TATTACTAATTCTAGCTTTATTACTCTTAGTATTATTCACACCTGACCTACTTGGAGACC 360
add.nas        TACTACTAATTCTAGTCCTCATACTACTAGTATTATTCACACCCGACCTACTTGGAGACC 350
ory.dam        TACTACTAATCCTAGCCCTTATGTTGCTAGTATTATTCGCACCCGACCTACTTGGAGACC 360
hip.equ        TACTACTAATTCTAGCCCTCATACTACTAGTACTATTCGCACCCGACCTACTTGGAGACC 360
alc.bus        TATTACTAATCCTAGCCCTCATACTACTAGTACTATTCGCACCCGACCTGCTCGGAGACC 360
sig.lic        TATTACTAATTCTAGCCCTCATACTACTAGTACTATTCGCACCCGACCTGCTCGGAGACC 360
bea.hun        TACTACTAATTCTAGCCCTCATATTACTAGTACTATTTGCACCCGACCTGCTCGGAGACC 350
dam.lun        TACTACTAATTCTAGCCCTCATACTACTAGTACTATTTGCACCCGACCTGCTCGGAGACC 350
con.tau        TATTACTAATTCTAGCCCTAATACTACTAGTACTATTCGCGCCCGATTTACTTGGAGACC 360
amm.ler        TGCTACTAATCCTCACCCTCACACTACTAGTACTATTTACACCCGATCTACTCGGGGACC 350
pse.nay        CACTGCTAATCCTCGCCCTGATATTACTAGTATTATTTACACCCGACCTACTCGGAGACC 360
cap.ibe        TGCTACTAATTCTTGTCCTAATATTACTAGTACTATTCACACCCGACCTACTCGGGGACC 360
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rup.pyr        TACTACTAATCCTCACCCTTATACTACTGGTACTATTTACACCTGACCTACTCGGAGACC 360
rup.rup        TACTACTAATCCTCACCCTCATACTACTAGTACTATTNACACCTGACCTACTCGGAGACC 350
nem.cau        TACTACTAATCCTCACCCTTATTTTACTGGTATTATTCACACCTGACTTACTTGGAGATC 360
bud.tax.tax    TACTACTAATCCTCGTCCTCATGTTGCTAGTACTATTTATACTTGACGTACTTGGAGACC 360
pan.hod        TACTACTAATCCTAATCCTCATATTACTAGTACTATTTTCACCCGACCTACTCGGAGACC 350
ovi.amm        TCCTACTAATCCTCACCCTCATACTACTAGTACTATTCACGCCTGACCTACTCGGAGACC 360
ovi.vig        TCCTACTAATCCTCATCCTCATGCTGCTAGTACTATTCACGCCTGACTTACTTGGAGACC 360
cap.cri        TGCTACTAATCCTCACCCTCATACTACTAGTACTGTTCACACCCGACCTACTCGGAGACC 360
ovi.mos        TACTACTAATCCTTACCCTTATACTACTAGTATTATTCACACCCGACCTACTTGGAGACC 360
ore.ame        TACTACTCATCCTCACCCTTATACTACTAGTATTATTCTCACCCGACTTACTCGGAGACC 350
cep.dor        TACTACTCATTCTAGCCCTAATAATCCTAGTATTATTCTCACCCGACTTACTTGGAGACC 360
cep.max        TATTACTTATTCTAGCCCTAATAATCCTAGTACTATTCTCACCCGACTTACTCGGAGATC 350
bis.bon        TATTACTAATTCTAACTCTAATACTACTAGTACTATTCGCACCGGACCTCCTCGGAGACC 350
bos.gru        TATTACTAATTCTAGCCCTAATACTTCTGGTACTATTCACACCCGACCTCCTCGGAGACC 360
bos.tra        TACTACTTATTCTAGCCCTAATAATACTAGTACTATTCGCACCCGACCTCCTCGGAGACC 350
bub.min        TGCTATTAATCCTAGCCCTAATACTATTAGTACTATTCACACCCGACCTCCTCGGGGACC 350
buba.bub       TACTATTAATCCTAGCCCTAATACTATTAGTACTATTCGCACCCGACCTCCTCGGGGACC 360
tra.ang        TACTATTAATCCTAGCCCTAATAGTACTAGTACTATTCACACCTGACCTCCTCGGAGACC 350
tra.eur        TACTGCTAATCCTAACTCTAATACTCCTAGTACTATTCGCACCCGACCTTCTCGGAGACC 350
kob.ell        TACTACTAATCCTAGTCCTAATACTCCTAGTTCTATTCGCCCCCGACCTACTTGGAGATC 350
kob.meg        TCCTATTAATCCTAATACTAATACTCCTAGTACTATTTGCCCCCGACCTACTTGGAGACC 360
red.aru        TACTGCTAATCCTAGTCCTAATGCTCTTAGTATTATTCACCCCTGACCTACTCGGAGATC 350
red.ful        TACTACTAATCCTGGCCCTAACACTATTAGTACTATTCACCCCTGACCTACTCGGAGACC 350
neo.mos        TCCTACTAATTCTAGTGCTAACACTCTTAGTTTTATTTGCACCTGACCTTTTAGGAGACC 350
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our.our	TCCTACTAATTCTAGCCCTCATGCTCCTAGTCCTATTCACACCAGACCTGCTTGGAGACC	360
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mad.kir	TACTACTAATTATAGGCCTCATACTCCTAGTTCTATTCTCACCAGACCTGCTCGGAGACC	360
rap.mel	TCCTATTAATCCTAACCCTTATGCTTCTAGTTCTATTCGCACCAGACCTACTCGGAGACC	360
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hyd.ine	TCCTTCTAATTCTTTTCCTAATGTTATTAGTCCTATTTTCACCTGACCTGCTTGGAGACC	360
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cer.dam	TATTCCTATTTCTCTTCTTAATAACACTAGTACTATTTGCACCAGACTTACTAGGAGACC	360
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mos.chr	TATTACTAATCCTAGTCTTAATAACACTAGTACTATTCACACCTGATTTACTTGGAGACC	360
mos.ber	TAATACTAATCTTAGTCTTAATAGTACTAGTACTATTCACACCCGATTTACTTGGAGACC	360
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trag.nap	TAGTCCTAATACTAGTCCTTCTATTACTAGTCCTATTTTCACCGGACTTGTTGGGAGACC	360
bala.acu	TACTACTAATTCTAACCCTACTAGCACTAACCCTATTCGCACCGGACCTGCTTGGAGACC	360
bala.bon	TACTACTAATTCTAACCCTACTAACACTAACCCTATTCGCACCCGACCTGCTCGGAGACC	360
bala.bor	TACTACTAATCCTAACCCTACTAATACTAACCCTATTCGCACCCGACCTGCTTGGAGACC	360
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esch.rob	TGCTACTAATCCTAACCCTACTAATACTAACCCTATTCGCACCCGACCTGCTCGGAGACC	360
bala.mus	TACTACTAATCCTAACCCTACTAATATTAACTCTATTTGCACCCGACTTACTCGGAGACC	360
mega.nov	TATTACTAATCCTAACCCTACTAATGTTAACCCTATTCGCACCTGACCTGCTTGGAGACC	360
bala.phy	TATTACTAATCCTAATCCTACTAATACTAACCCTATTCGCACCCGACCTACTTGGAGACC	360
cap.mar	TACTACTAATCCTGACCCTACTAATATTAACCTTATTTACACCTGACCTGCTTGGAGACC	360
ceph.com	TATTCCTAATCCTAACCCTACTAGCATTAACCCTATTTGCCCCCGACCTACTAGGAGACC	360
ceph.eut	TATTCCTAATCCTAACCCTACTAGCACTAACCCTATTCGCCCCTGACCTACTAGGAGACC	360
lage.obl	TATTCCTAATTCTAACCCTACTAGCACTAACCCTATTCACCCCTGACCTACTAGGAGACC	360
ceph.hea	TATTCCTAATTCTAGCCCTACTAGCACTAACCCTATTCGCCCCTGACCTACTGGGAGACC	360
ceph.hec	TATTCCTAATTCTAATCCTACTAGCACTAACCCTATTCGCCCCTGACCTACTAGGAGACC	360
lage.aus	TATTCCTAATTCTAGCCCTACTAGCACTAACCCTATTCACCCCTGACCTACTAGGAGACC	360
lage.cru	TATTCCTAATCCTAACCCTACTAGCACTAACCCTGTTCACCCCTGACCTACTAGGAGACC	360
lage.obs	TATTCCTAATTCTAGCCCTACTAACACTAACCTTATTCACCCCCGACCTACTAGGAGACC	360
lisso.bor	TATTCTTAATTCTGGCCCTACTAGCACTAACCCTATTCACCCCTGACCTATTAGGAGATC	360
lisso.per	TATTCTTAATTCTGACCCTACTAGCACTAACCCTATTTACCCCTGACCTGTTAGGAGACC	360
glo.mac	TACTCTTAATCCTAGCACTACTAACACTAACCCTATTCACCCCTGACCTACTAGGAGACC	360
glo.mel	TACTCTTAATCCTAGCACTACTAACACTAACCCTATTCACCCCTGACCTACTAGGAGACC	360
fere.att	TACTCTTAATTCTAACATTACTAACACTAACCCTGTTCACCCCTGACCTACTAGGAGACC	360
pepo.ele	TACTCTTAATCTTAGCACTACTAACACTAACCCTATTCACCCCTGACCTACTAGGAGACC	360
gram.gri	TACTCCTAATCCTAACACTACTAACACTAACCCTATTCACCCCTGACCTACTAGGAGACC	360
pse.cra	TACTCTTAATTCTAACACTACTAACACTAACCCTATTCACCCCCGACCTACTAGGAGACC	360
lage.acu	TACTCTTAATTCTAACCCTACTAGCACTAACCCTATTCACCCCTGACCTACTAGGAGACC	360
orci.bre	TACTCTTAATCCTAACCCTGCTAGCACTAACCTTATTTGCCCCTGACCTACTAGGAGACC	360
orca.bre	TACTCTTAATCTTAGTCCTACTAACACTAACCCTGTTCACCCCCGACCTACTAGGAGACC	

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del.tro	TACTCCTAATCTTAACCTTACTAGCACTGACCCTATTCACTCCCGACCTACTAGGAGACC	360
del.del	TACTCCTAATCTTAACCCTACTAGCACTAACCCTATTCACTCCCGACCTACTAGGAGACC	360
sten.cly	TACTCCTAATCTTAACCCTACTAGCACTAACCCTATTCACCCCCGACCTACTAGGAGACC	360
sten.coe	TACTCCTAATCTTAACCCTACTAGCACTAACCCTATTCACCCCCGACCTACTAGGAGACC	360
tur.adu	TACTCCTAATCTTAACCCTACTAGCACTAACCCTATTCACCCCCGACCTACTAGGAAACC	360
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saus.chi	TACTCCTAATCTTAACCCTACTAGCACTAACCCTATTCACCCCCGACCTACTAGGAGACC	360
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lage.alb	TACTTTTAATCCTAACCTTACTAGCACTAACCCTATTTACCCCCGACCTACTAGGAGATC	360
sten.bre	TACTTTTAATCCTAACTTTACTAGCACTAACCCTATTCACCCCCGACCTACTAGGAGACC	360
sota.flu	TACTCCTAATCCTGACCCTACTAGCACTAACCCTATTCACCCCCGACCTACTAGGAGATC	360
del.leu	TACTACTAATCCTAACCCTATTAACAGTAACCCTATTCACACCTGACCTCCTAGGAGACC	360
mono.mon	TCCTACTAATCCTAATTCTACTAGCAATAACCCTACTCACACCTGACCTCCTAGGAGACC	360
plat.gan	TCATCCTAATCCTAACCTCACTCACATTAACCTTATTTACACCTGACCTACTAGGAGACC	360
plat.min	TCATCCTAATCCTAACCTCACTCACATTAACCTTATTTACACCTGACCTACTAGGAGACC	360
kogi.bre	TACTGCTAATCTCAGCGCTACTTACATTAACCCTATTCGCACCAGACCTATTAGGAGACC	360
kogi.sim	TACTACTAATCTCAGCACTACTCACACTGACCCTGTTCGCACCTGATCTACTAGGAGACC	360
phys.cat	TACTACTAATCCTATCCCTACTTACACTAACCCTGTTCGCACCCGACCTGCTAGGAGATC	360
lipo.vex	TTCTATTAATATTTGTTCTACTCACACTAACCTTACTTGCACCAGACCTACTCGGAGATC	360
phoc.sin	TACTATTTATTCTAACTTTACTAACACTAACCTTATTTTTACCTGACCTTCTAGGAGACC	360
bera.bai	TACTACTAATCCTAGCCCTACTCACGCTAACCCTATTTGCACCCGACCTACTAGGAGAGC	360
ziph.car	TACTATTAATCGTAATTCTACTCGCACTAACCCTATTCGCACCCGACCTGCTAGGAGACC	360
meso.eur	TACTACTAATTCTAGCCCTACTCACCCTAACCCTATTCGCACCCGACCTGCTAGGAGACC	360
meso.bid	TACTACTAATTCTAACCCTACTCGCACTAACCCTATTCGCACCTGACCTGCTAGGAGACC	360
meso.den	TACTATTAATTCTGGCCCTACTTATACTAACCCTATTTGCACCTGACCTACTAGGAGACC	360
hype.amp	TATTACTAATCCTAGTCCTACTCACATTAACCCTATTCGCACCCGACCTACTAGGAGACC	360
meso.per	TATTATTAATTATAGTCCTACTTATACTAACCCTATTTGCACCTGACCTATTAGGAGATC	360
pont.bla	TATTAATAATCCTAACAATACTCACGCTGACTCTATTCACCCCTGACCTATTAGGAGACC	360
hex.lib	TACTTCTAATAACAATACTACTCACACTAACCTTATTTGCCCCAGACCTCCTAGGGGACC	360
hipp.amp	TACTCCTAATAACAACACTACTCACACTAACCTTATTTGCCCCAGACCTCCTAGGGGACC	360
dic.sum	TACTTCTAATCCTAGCCCTACTCACCCTAGTTCTATTCTCGCCTGACCTCCTAGGAGACC	360
rhin.son	TGCTTCTAATTATAGTATTACTCACCCTAGTCCTATTCTCCCCTGACATCCTAGGGGACC	360
cera	TACTCCTAATCCTAGCACTACTCGCCCTAGTTCTATTCTCACCAGACATCCTAGGAGACC	360
equu	TCCTCCTAGTCCTACTCCTACTAACCCTAGTATTATTCTCCCCTGACCTCCTAGGAGACC	360
baby.bab	TACTCATAATTATAGCTCTTCTAATCCTAGTACTATTCTCACCAGATCTACTAGGAGACC	360
phac.afr	TATTCATAATACTAATCCTGCTAATCCTAGTATTATTCTCCCCAGACCTACTAGGAGACC	360
sus.bar	TATTTATAATACTAATCCTACTAATCTTAGTACTATTCTCACCAGACCTACTAGGAGACC	360
sus.scr.ewb3	TATTTATAATACTAATCCTACTAATCCTTGTACTATTCTCACCAGACCTACTAGGAGACC	360
lama.gla	TACTACTTATTCTAACCCTACTTCTACTCGTACTATTCTCACCAGACCTACTAGGAGACC	360
lama.gua	TACTACTTATTCTGACCCTACTTCTACTCGTACTATTCTCACCAGACCTACTAGGAGACC	360
vic.vic	TACTACTTATTCTGATTCTACTCCTACTCGTACTATTCTCACCAGACTTACTAGGAGACC	360
cam.bac	TGCTACTAATATTAATTCTGCTTATTCTCGTACTGTTCTCACCAGACTTATTAGGAGATC	360
arc.for	TCCTACTAATCTTGATTCTAATATTACTAGTAATATTTTCACCAGATCTGCTGGGAGACC	360
arc.gaz	TCTTACTAATCTTAATTCTAATATTACTAGTAATATTTTCACCAGATCTGCTAGGAGACC	360
eum.jub	TCCTACTAATCTTAATCCTAATACTACTAGTAATATTTTCACCAGACCTGCTGGGAGACC	360
zal.cal	TCCTACTAATCTTAACCCTAATACTACTAGTAATATTTTCACCCGACCTGCTGGGAGACC	360
odo.ros	TCATTCTAATCCTAATCCTAATACTACTAGTACTATTCTCACCAGATTTACTGGGAGACC	360
pho.fasciata	TACTCCTCATCCTAGTCCTAATACTACTAGTACTATTCTCACCCGACCTACTAGGAGACT	360
pho.gro	TACTCCTCATCCTGGTCCTTATACTACTAGTACTGTTCTCACCCGACCTACTGGGAGACC	360
pho.vit	TACTTCTCATTCTAGTCCTGACACTACTAGTGCTATTCTCACCCGACCTGTTAGGAGACC	360
cys.cri	TACTCCTCATCCTAGTTCTAACACTACTAGTGCTATTCTCACCCGATCTGCTAGGAGACC	360
hyd.lep	TATTCCTCATTCTAACCCTAATACTACTAGTATTATTCTCACCCGACCTACTAGGAGACC	360
lep.wed	TACTCCTCATTCTAACCCTAATATTACTAGTATTATTCTCACCCGACCTGCTAGGAGATC	360
mir.leo	TACTTCTTATTCTAACCCTAATACTATTAGTGTTATTCTCACCCGACTTATTAGGAGACC	360
tri.bar	TACTTCTAATCCTAGTTCTTATACTTCTAGTGCTATTCTCACCCGACCTACTGGGAGATT	[illegible]
pon.gch	TACTCCTTATCCTAATTCTAATATTACTAGTATTATTCTCACCCGACTTACTAGGAGACT	

hela.mal	TACTTCTTACCCTAGCCCTAACAACCCTAGTTCTATTCTCGCCCGACTTACTAGGAGACC	360
sel.thi	TACTTCTCATCCTAGCCTTAGCAACTCTAGTCCTATTCTCGCCCGACTTACTAGGAGACC	360
ail.ful	TACTCCTTATCCTAATTCTCATGACATTAGTACTATTCTTACCTGACTTGCTTGGTGATC	360
fel	TAGTACTAGTTTTAACACTCATACTACTCGTCCTATTTTCACCAGACCTGCTAGGAGACC	360
can	TACTCCTACTCCTAATCCTAATATCACTAGTTTTATTTTCACCTGACCTATTAGGAGACC	360
tal	TAATCCTAATTATAGCTCTATCATCATTAGTATTATTTTCACCTGACCTACTAGGAGACC	360
gla.sab	TAATCCTCATCTTAATCTTCATAACCCTAGTTCTCTTCACCCCTGATCTTCTAGGAGACC	360
gla.vol	TAATCCTTATCTTAATCTTCATAACCCTAGTTCTCTTCACCCCGGATCTTCTAGGAGACC	360
hyl.pha	TTATTCTTCTCCTAATCTTTATAAACTTAGTACTATTTTCCCCCGATCTTTTAGGAGACC	360
pet.set	TTATTCTTCTCCTAATCTTTATAAACTTAGTACTATTCTCCCCCGATCTTTTAGGAGACC	360
bel.pea	TAATCTTCGGCCTTATATTTACAACCCTTATTCTATTCGCCCCTGATCTCCTAGGAGACC	360
pte.mom	TTCTCCTTGGCCTCCTATTCATAATCTTAGTCCTCTTTACTCCAGACCTCCTTGGAGACC	360
gala.demi	TTATTCTCTTACTAACTCTGTTCTCCCTAGTAATATTCTCCCCGGACCTGCTAGGAGACC	360
pero.pot	TCTTTCTTCTACTAATCCTACTCACCCTAGTCCTATTCTCCCCAGACCTATTAGGAGACC	360
gala.mat	TCTTCTTACTACTATGCCTATTCTCTCTAGTACTATTTTCCCCCGATCTGTTAGGAGACC	360
gala.moh	TCCTCTTACTATTATCCCTATTCTCTCTAGTACTATTCTCCCCTGACCTGCTGGGAGACC	360
oto.gar	TCCTCCTCCTTCTAACCCTATTCTGCCTAGTCCTATTCTCCCCCGACCTTCTAGGAGACC	360
lor.tar	TTGCTCTCTTAATCACCTTATCAACTCTAGTTCTATTCTCCCCTGACCTTTTAGGAGACC	360
nyc.cou	TTTTCCTATTAGCAACCCTATCTATTCTAGTCTTATTCTCCCCTGACCTCCTAGGAGACC	360
mus	TAATCATATTCTTAATTCTCATAACCCTAGTATTATTTTTCCCAGACATACTAGGAGACC	360
gorr	TCCTCTTTCTCCTGACCTTGATAACATTAACACTATTCTCACCAGACCTCCTAGGAGACC	360
homo	TTCTCTTCCTTCTCTCCTTAATGACATTAACACTATTCTCACCAGACCTCCTAGGCGACC	360
dug.dug	TCCTCCTCATTCTAGTCTTACTCCTACTAACCCTGTTCTCCCCGGACATACTGGGAGACC	360
ele.max	TTATCCTAATTTTACTCCTTCTACTCTTAGCCCTACTATCTCCAGACATACTAGGAGACC	360
afr.con	CACTCATGCTCATTCCATTCCTGACACTAGCCCTACTCTCCCCCAACCTCTTAGGTGATC	360
pavo.mut	CTCTTATATTTATCCCATTCCTAACACTAGCCCTATTCTCCCCCAATCTCCTAGGTGACC	360
tra.bly	CACTCATGCTCACCCCCCTCCTCACACTAGCATTATTCTCACCGAACCTATTAGGCGACC	360
tra.sat	CACTCATGCTCACCCCCCTCCTCACACTAGCCTTATTCTCACCAAACCTACTAGGTGATC	360
tra.cob	CACTCATACTCACTCCTCTCCTCACACTAGCCTTATTTTCACCAAACCTACTAGGTGACC	360
tra.tem	CACTCATACTCACTCCCCTCCTCACACTAGCCTTATTTTCACCAAACCTACTAGGTGATC	360
arg.arg	CACTCATACTCGCTCCATTCCTTACACTAACCCTATTCTACCCAAACCTACTAGGTGACC	360
cat.wal	CACTTATATTCACCCCATTCCTAACACTAGCCCTATTCTCACCAAATCTTCTGGGCGACC	360
cro.cro	CACTTATACTCACCCCATTCCTAACACTAGCCCTATTCTCACCTAACCTTCTGGGCGACC	360
sym.ree	CACTTATACTCACCCCATTCCTCACACTAGCCCTATTCTCACCTAACCTGCTAGGCGACC	360
bam.tho	CCCTTATATTCATCCCATTCCTGACACTAGCCCTATTCTCCCCTAACCTCCTAGGAGACC	360
fra.fra	CCCTTATATTCATCCCTCTCCTTACACTAGCCCTATTCTCCCCCAACCTCCTAGGCGACC	360
ith.cru	CACTTATACTCATCCCCTTTCTTACACTAGTCCTATTTTCCCCCAACCTCCTAGGAGATC	360
ant.par	TACTCATACTACTCCCACTCATAACCCTAGCTCTATTCTCACCAAACTTACTAGGAGACC	360
ant.vir	TACTCATACTACTCCCACTCATAACCCTAGCTCTATTCTCACCAAACTTACTAGGAGACC	360
gru.ant.ant	CACTCATACTACTTCCACTCATAACCCTAGCCCTATTCTCACCAAACCTACTAGGAGACC	360
gru.ant.gil	CACTCATACTACTTCCACTCATAACCCTAGCCCTATTCTCACCAAACCTACTAGGAGACC	360
gru.ant.sha	CACTCATACTACTTCCACTCATAACCCTAGCCCTATTCTCACCAAACCTACTAGGAGACC	360
gru.leu	TACTCATACTACTTCCACTCATAACCTTAGCCCTATTCTCACCAAACTTACTAGGAGACC	360
gru.can.pra	TACTCATACTACTTCCACTCATAACCCTAGCTCTATTTTCACCAAACTTACTAGGAGACC	360
gru.can.row	TACTCATACTACTTCCACTCATAACCCTAGCTCTATTTTCACCAAACTTACTAGGAGACC	360
gru.can.tab	TACTCATACTACTTCCACTCATAACCCTAGCTCTATTTTCACCAAACTTACTAGGAGACC	360
gru.can.can	TACTCATACTACTTCCACTTATAACCCTAGCTCTATTCTCACCAAACTTACTAGGAGACC	360
gru.ame	CACTCATATTACTTCCACTCATAACCCTAGCTCTATTTTCACCAAACTTACTAGGAGACC	360
gru.gru	TACTCATATTACTTCCACTCATAACCCTAGCTCTATTTTCACCAAACTTACTAGGAGACC	360
gru.mon	TATTCATATTACTTCCACTCATAACCCTAGCTCTATTTTCACCAAACTTACTAGGAGACC	360
gru.nig	TATTCATATTACTTCCACTCATAACCCTAGCTCTATTTTCACCAAACTTACTAGGAGACC	360
gru.jap	CACTCATATTACTTCCACTCATAACCCTAGCCCTATTCTCACCCAACCTACTAGGTGACC	360
cic.boy	CACTCCTACTTTTGCCACTAACCACTCTGGCCCTATTCTCACCCAACCTCCTAGGGGACC	360
che.ame	CTCTCATATTTATCCCGCTCCTAACCCTAGCCTTCTTCTCACCCAACCTACTAGGAGACC	360
ant.alb	CAGTAATACTCCTCCTCCTAACCTCCCTAGCCCTTTTCTCCCCCAACCTACTAGGAGACC	360
fal.fam	TACTCATATACCTTCCCCTAATAACCTTAGCCCTATTCACTCCCAACCTACTAGGAGACC	360
fal.ves	TACTCATATACCTTCCCCTAATAACCCTAGCCCTATTTACCCCAAACTTACTAGGAGACC	360
fal.per	TACTCATATACCTTCCCCTAATAACCCTAGCCCTATTTACCCCAAACCTGCTAGGAGACC	

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fal.spa        TGCTCATACTCCTGCCCCTAATAGCCCTAGCCCTATTCACCCCAAACCTGCTAGGAGACC 360
ayt.ame        TCCTCATGCTCACCCCCCTAATAGCACTAGCCCTATTCTCACCAAACCTCCTAGGAGACC 360
smi.sha        CAATCATACTAACACCACTAATAACCCTAGCCATATTCTCTCCTAACCTCCTAGGAGACC 360
vid.cha        TACTAATATTCGCACTCCTAGCTTCCATAGCCCTATTCTCCCCAAACATACTAGGAGATC 360
chry.pic       TTCTAATACTAACCCTCCTACTAACCCTAACACTATTCTCTCCAAACCTTTTAGGGGACC 360
emy.orb.kur    TCCTAATACTAGCCTTCCTGCTAACCCTAACACTATTCTCTCCTAACCTTCTAGGAGACC 360
che.mud        TTTTAATACTAACTTTCCTCCTAACCTTAACACTTTTCTCCCCCTACTTACTAGGAGACC 360
eum.egr        TCATTATACTGTCTGTTCTACTAGCCCTCGCCCTTTTCTCACCAAACCTTCTAGGCGACC 360
                  *                     *      *  *     *    *   *   * **   * *

aep.mel        CAGACAANNACATCCCCGCAAACCCACTCAACACCCCTCCCCACATCAAGCCCGAATGGT 420
ore.ore        CAGATAACTACACCCCAGCAAACCCACTCAACACTCCCCCTCACATTAAACCAGAATGGT 420
add.nas        CAGACAATTATACCCCAGCAAATCCACTTAGCACGCCCCCTCACATCAAACCTGAATGAT 420
ory.dam        CAGATAATTATACACCAGCAAATCCACTTAACACACCCCCTCACATCAAACCCGAATGAT 420
hip.equ        CAGACAACTATGCCCCAGCAAACCCACTCAACACGGCCCCTCACATTAAACCCGAATGAT 420
alc.bus        CAGACAACTACACCCCCGCGAACCCACTTAACACACCCCCTCACATCAAGCCCGAATGAT 420
sig.lic        CAGACAACTACACCCCCGCGAACCCACTTAACACACCCCCTCACATCAAGCCCGAATGAT 420
bea.hun        CAGACAACTACACCCCCGCAAACCCACTTAATACACCCCCTCACATCAAACCCGAATGAT 420
dam.lun        CAGACAACTACACCCCTGCAAACCCACTCAACACGCCCCCTCACATCAAGCCCGAGTGAT 420
con.tau        CAGACAACTACACCCCCGCAAATCCACTCAACACACCCCCTCACATCAAGCCCGAATGAT 420
amm.ler        CAGACAACTATACCCCAGCAAATCCACTCAACACACCCCCTCATATTAAACCTGAATGAT 420
pse.nay        CAGACAACTACACCCCAGCAAACCCACTCAACACACCCCCTCACATTAAACCCGAGTGAT 420
cap.ibe        CAGACAACTATACCCCAGCAAACCCACTCAATACACCCCCTCACATTAAACCTGAATGAT 420
hem.jem        CAGACAACTATACCCCAGCAAATCCACTCAACACACCCCCTCACATTAAACCTGAATGAT 420
cap.fal        CAGATAACTATATCCCAGCAAATCCACTCAATACACCCCCTCATATCAAACCTGAGTGGT 420
rup.pyr        CAGATAACTATACCCCAGCGAACCCACTCAACACACCCCCTCACATCAAACCCGAATGAT 420
rup.rup        CAGATAATTACACCCCAGCGAACCCACTCAACACACCCCCTCACATTAAACCCGAGTGAT 420
nem.cau        CAGACAACTATACCCCAGCAAACCCACTCAGCACACCCCCTCACATTAAACCTGAATGAT 420
bud.tax.tax    CAGATAATTATACCCCAGCAAATCCACTCAACACACCCCCTCACATCAAACCTGAATGAT 420
pan.hod        CAGACAATTATACCCCAGCAAACCCCCTCAACACACCACCCCACATTAAACCTGAATGGT 420
ovi.amm        CAGACAACTACACCCCAGCAAACCCACTTAACACTCCCCCTCACATCAAACCTGAATGAT 420
ovi.vig        CAGACAACTACACCCCAGCAAACCCACTTAACACTCCCCCTCACATCAAACCTGAATGAT 420
cap.cri        CAGACAACTACACTCCAGCAAACCCACTCAACACACCCCCTCACATCAAGCCCGAGTGAT 420
ovi.mos        CAGACAACTATACCCCAGCAAACCCACTCAACACACCCCCTCACATTAAACCAGAGTGAT 420
ore.ame        CAGACAACTACACTCCAGCAAACCCGCTAAATACACCTCCCCATATCAAGCCCGAATGAT 420
cep.dor        CAGATAACTACACCCCAGCAAACCCACTCAACACACCTCCCCATATTAAACCCGAATGAT 420
cep.max        CAGATAATTATACTCCAGCAAACCCACTTAACACACCTCCCCACATCAAGCCCGAATGAT 420
bis.bon        CAGATAACTACACCCCAGCAAATCCACTTAACACACCTCCCCACATCAAACCCGAATGAT 420
bos.gru        CAGACAACTACACCCCAGCAAATCCACTCAACACACCTCCCCACATCAAACCCGAATGAT 420
bos.tra        CAGACAACTACACCCCAGCAAACCCACTTAGCACACCTCCCCATATTAAGCCCGAATGGT 420
bub.min        CAGACAACTACACCCCAGCAAACCCACTCAACACACCTCCCCATATCAAACCTGAATGGT 420
buba.bub       CAGACAACTACACCCCAGCAAACCCACTCAACACACCTCCCCACATCAAGCCTGAATGGT 420
tra.ang        CCGACAACTACACCCCAGCGAACCCCCTCAATACACCTCCCCATATCAAACCTGAATGAT 420
tra.eur        CCGACAACTACACCCCAGCAAACCCACTCAACACACCACCTCATATCAAACCTGAATGAT 420
kob.ell        CTGACAACTATGCCCCAGCAAACCCACTTAACACGCCCCTCACAATTAAACCTGAATGAT 420
kob.meg        CTGACAATTATACCCCAGCAAACCCACTTAATACACCTCCCCATATTAAACCCGAATGAT 420
red.aru        CCGACAATTATACTCCAGCAAATCCACTCAACACACCCCCTCATATTAAACCCGAATGAT 420
red.ful        CGGACAATTACACCCCAGCAAACCCACTCAACACACCCCCTCACATCAAACCAGAATGGT 420
neo.mos        CAGACAACTACACCCCCGCAAACCCTCTTAACACGCCTCCCCATATCAAACCCGAATGAT 420
pel.cap        CTGACAATTACACCCCTGCAAACCCGCTCAACACACCCCCTCATATCAAACCCGAATGAT 420
gaz.dam        CAGACAACTACACACCAGCAAATCCACTCAATACACCCCCACATATTAAGCCTGAGCGAT 420
our.our        CAGACAACTATACACCAGCAAACCCACTAAATACACCCCCACATATTAAACCTGAGTGGT 420
ant.cer        CAGACAACTATACACCAGCAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT 420
sai.tat        CAGACAACTACACRCCAGCAAACCCACTTAACACACCCCCACATATTAAACCCGAATGAT 420
mad.kir        CAGACAACTACACACCAGCAAATCCCCTTAACACGCCCCCACACATTAAACCTGAATGAT 420
rap.mel        CAGACAACTATACACCAGCAAACCCACTCAACACACCCCCACATATCAAACCCGAATGGT 420
gaz.gaz        CAGACAACTATACACCAGCAAATCCACTCAACACACCCCCACACATCAAACCTGAATGGT 420
ant.ame        CCGACAACTACACACCAGCTAACCCACTCAACACTCCCCCACACATTAAGCCAGAATGAT 420
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turs.tru	CTGATAACTACACCCCAGCAAACCCACTAAGCACCCCTGCACACATCAAACCAGAATGAT	420
lage.alb	CCGATAACTATACCCCAGCAAATCCACTAAGCACTCCTGCACACATCAAACCAGAATGGT	420
sten.bre	CCGACAACTATACCCCAGCAAATCCACTAAGCACCCCTGCACACATCAAACCAGAATGGT	420
sota.flu	CCGACAACTATACTCCAGCAAATCCACTTAACACCCCTGCACACATCAAACCAGAATGAT	420
del.leu	CAGACAATTACACCCCAGCAAACCCACTAAACACCCCCGCACACATCAAACCAGAATGGT	420
mono.mon	CTGACAATTATACCCCAGCAAACCCACTAAGCACCCCTGCACACATCAAACCAGAATGAT	420
plat.gan	CCGATAACTACACCCCAGCAAACCCGCTTAATACCCCAGCACATATCAAACCAGAGTGAT	420
plat.min	CCGATAACTACACCCCAGCAAACCCGCTTAATACCCCAGCACATATCAAACCAGAGTGAT	420
kogi.bre	CTGACAACTACACCCCAGCAAACCCACTAAGCACCCCGGCACACATTAAACCAGAATGAT	420
kogi.sim	CCGACAACTATACCCCAGCAAACCCACTAAGCACCCCCGCACACATTAAACCAGAATGAT	420
phys.cat	CTGACAACTACACCCCAGCAAATCCACTAAATACCCCAACACACATCAAACCAGAATGGT	420
lipo.vex	CTGATAATTATACCCCAGCAAACCCACTAAACACTCCCGCACACATCAAACCAGAATGAT	420
phoc.sin	CCGATAACTACATTCCAGCAAACCCACTAAGCACCCCAGCACACATTAAACCAGAATGAT	420
bera.bai	CCGACAACTATACCCCGGCAAACCCGCTCAGCACCCCAACACATATTAAGCCAGAATGAT	420
ziph.car	CCGATAACTATACCCCAGCAAATCCACTCAGCACCCCAGCACACATTAAGCCAGAATGAT	420
meso.eur	CCGACAATTACACCCCAGCAAACCCACTTAATACTCCAGCACACATCAAACCAGAATGAT	420
meso.bid	CCGACAACTATACCCCAGCAAACCCACTCAGCACCCCAGCCCACATCAAACCAGAGTGGT	420
meso.den	CCGATAATTATACTCCAGCAAACCCACTCAACACTCCAGCACACATCAAACCAGAGTGGT	420
hype.amp	CTGATAACTATACCCCAGCAAACCCACTCAGCACTCCAGCACACATCAAACCAGAATGGT	420
meso.per	CTGACAATTACACTCCAGCAAACCCACTTAGCACCCCAGCACATATTAAACCAGAATGAT	420
pont.bla	CAGACAACTATATCCCAGCAAACCCCATGAATACCCCAGAGCACATTAAACCAGAATGGT	420
hex.lib	CAGACAACTACACCCCCGCAAACCCCCTTAGCACACCACCACACATCAAACCAGAATGAT	420
hipp.amp	CAGACAACTACACCCCCGCAAACCCCCTTAGCACACCACCACACATTAAACCAGAATGAT	420
dic.sum	CGGACAACTACACACCCGCCAACCCTCTCAGCACCCCTCCACACATTAAACCAGAATGGT	420
rhin.son	CAGACAACTACATCCCAGCCAACCCTCTCAGCACCCCTCCACATATCAAACCAGAATGGT	420
cera	CTGACAACTACACCCCTGCCAATCCTCTCAGCACTCCCCCACATATCAAACCAGAATGAT	420
equu	CAGACAACTACACCCCAGCTAACCCCCTCAGCACTCCCCCTCATATTAAGCCAGAATGGT	420
baby.bab	CGGACAACTATACTCCAGCAAACCCACTAAATACACCACCCCACATTAAGCCAGAATGAT	420
phac.afr	CAGACAACTATACCCCAGCAAACCCATTAAACACACCACCCCACATCAAACCAGAATGAT	420
sus.bar	CAGACAACTACACCCCAGCAAACCCACTAAACACCCCACCCCATATTAAACCAGAATGAT	420
sus.scr.ewb3	CAGACAACTACACCCCAGCAAACCCACTAAACACCCCACCCCATATTAAACCAGAATGAT	420
lama.gla	CCGACAACTATACTCCCGCTAACCCCCTCAACACACCGCCCCATATTAAACCAGAATGAT	420
lama.gua	CCGACAACTATACTCCCGCTAACCCCCTCAACACACCGCCTCATATTAAACCAGAATGAT	420
vic.vic	CCGACAACTATACCCCCGCTAACCCCCTTAACACACCACCCCACATTAAACCAGAATGAT	420
cam.bac	CTGACAACTATACTCCCGCTAACCCCCTCAATACACCACCACACATTAAGCCGGAATGAT	420
arc.for	CAGACAACTACACCCCAGCCAACCCCCTCAGCACTCCACCACATATTAAACCTGAATGAT	420
arc.gaz	CAGACAACTACATCCCAGCCAACCCCCTCAGTACTCCACCACATATCAAACCTGAATGGT	420
eum.jub	CAGACAACTACATCCCAGCCAACCCCCTCAGCACTCCACCACATATTAAACCCGAATGAT	420
zal.cal	CAGACAACTATATTCCAGCCAACCCCCTCAGCACTCCACCACATATTAAACCTGAGTGAT	420
odo.ros	CGGACAATTACACCCCAGCCAACCCTCTCAGCACCCCACCCCATATCAAACCCGAATGAT	420
pho.fasciata	CCGACAACTACACCCCTGCCAACCCCCTAAGCACCCCACCACATATCAAGCCCGAATGAT	420
pho.gro	CCGACAACTACATCCCTGCCAATCCCCTAAGTACCCCACCACATATCAAGCCCGAATGAT	420
pho.vit	CCGACAACTATATCCCTGCCAATCCCCTAAGCACCCCACCACATATCAAACCTGAATGGT	420
cys.cri	CCGACAACTATACCCCTGCCAACCCCCTAAGTACCCCACCACATATTAAACCTGAATGAT	420
hyd.lep	CCGACAACTATATTCCTGCTAACCCCCTAAGCACCCCACCACATATCAAACCCGAATGAT	420
lep.wed	CCGACAACTATACTCCCGCTAATCCCCTAAGTACTCCACCACATATCAAACCCGAATGAT	420
mir.leo	CCGACAACTACACCCCTGCCAATCCCCTAAGCACCCCACCACATATTAAACCCGAATGAT	420
eri.bar	CCGACAACTACACTCCCGCTAACCCCCTAAGCACCCCACCACATATTAAGCCCGAATGAT	420
mon.sch	CTGACAACTACATCCCTGCCAACCCCTTAAACACTCCACCACACATTAAACCCGAATGAT	420
ela.mal	CTGACAACTACATCCCCGCAAATCCATTGAGCACCCCACCCCACATCAAACCCGAATGGT	420
el.chi	CTGATAACTATACCCCCGCAAACCCACTGAGCACCCCACCCCACATCAAACCCGAATGAT	420
il.ful	CTGATAACTATATTCCCGCTAACCCATTAAGCACACCACCCCATATTAAACCTGAGTGGT	420
el	CAGACAACTACATCCCAGCCAACCCTTTAAATACCCCTCCCCATATTAAACCTGAATGAT	420
an	CAGATAACTACACCCCTGCAAACCCCCTAAACACCCCTCCACATATTAAACCTGAGTGAT	420
al	CAGACAATTACATCCCGGCAAACCCGCTAAACACACCACTCCATATTAAACCCGAATGGT	420
la.sab	CAGACAACTATACCCCAGCCAACCCACTCAACACCCCTCCCCACATCAAACTAGAATGAT	420
la.vol	CAGACAACTATACTCCAGCCAACCCACTCAACGGCCCTCCCCATATCAAGCCAGAGTGAT	420
yl.pha	CTGACAACTACACCCCCGGCAACCCACTTAACACCCCTCCCCATATTAAACCAGAATGAT	

aep.mel	ACTTCCTGTTNGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
ore.ore	ATTTNCTATTNGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
add.nas	ATTTCCTATTTGCATACGCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
ory.dam	ATTTCCTATTTGCATATGCGATCTTACGATCAATCCCCAACAAACTAGGAGG	472
hip.equ	ATTTTTTATTCGCGTACGCAATTCTACGATCGATCCCCAATAAGCTGGGAGG	472
alc.bus	ATTTCCTATTTGCATATGCAATCCTACGATCAATCCCTAACAAACTAGGAGG	472
sig.lic	ATTTCCTATTTGCATACGCAATCCTACGATCAATCCCTAACAAACTAGGAGG	472
bea.hun	ATTTCCTATTTGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
dam.lun	ATTTCCTATTCGCATACGCAATCCTACGTTCGATCCCCAACGAGCTAGGAGG	472
con.tau	ACTTCCTATTTGCATATGCAATCCTACGATCAATCCCCAACGGACTAGGAGG	472
amm.ler	ACTTCCTATTTGCATACGCAATCCTACGATCAATCCCTAATAAACTGGGAGG	472
pse.nay	ACTTCCTATTTGCATACGCAATCCTACGATCAATTCCCAACAAGCTAGGAGG	472
cap.ibe	ATTTCCTATTTGCATACGCAATCCTACGATCAATTCCCAACAAACTAGGGGG	472
hem.jem	ATTTTCTATTTGCATACGCGATCCTACGATCAATTCCCAACAAACTAGGAGG	472
cap.fal	ACTTCCTATTTGCATACGCAATCCTACGATCAATCCCCAACAAACTAGGAGG	472
rup.pyr	ATTTCTTGTTTGCATATGCGATCCTACGATCAATTCCCAACAAACTTGGAGG	472
rup.rup	ATTTCTTATTTGCATATGCAATTCTACGATCAATCCCCAACAAACTTGGAGG	472
nem.cau	ATTTCCTATTTGCATATGCAATCTTACGATCAATCCCCAATAAACTAGGCGG	472
bud.tax.tax	ATTTCCTATTTGCATACGCAATCTTACGATCAATCCCCAACAAACTAGGAGG	472
pan.hod	ACTTTCTATTTGCATACGCAATCCTACGATCAATCCCCAACAAACTAGGAGG	472
ovi.amm	ACTTCCTATTTGCATACGCAATCTTACGATCAATCCCTAATAAACTAGGAGG	472
ovi.vig	ATTTCCTATTTGCATATGCAATCTTACGATCAATCCCTAATAAACTAGGAGG	472
cap.cri	ACTTCCTATTTGCATACGCAATCCTACGATCAATCCCCAACAAACTAGGCGG	472
ovi.mos	ACTTCCTATTTGCATACGCAATCCTACGATCAATTCCTAACAAACTAGGCGG	472
ore.ame	ACTTCCTATTTGCATACGCAATCTTACGATCAATCCCCAATAAACTAGGAGG	472
cep.dor	ACTTCCTATTTGCATACGCAATCCTACGATCAATTCCAAACAAACTAGGAGG	472
cep.max	ATTTCCTATTCGCGTACGCAATTCTACGATCAATTCCAAATAAATTAGGAGG	472
bis.bon	ACTTCTTATTTGCATANGCAATTTTACGGTCAATCCCCAACAAACTAGGAGG	472
bos.gru	ACTTCTTATTTGCATACGCAATTTTACGATCAATCCCCAATAAACTAGGAGG	472
bos.tra	ATTTCCTGTTCGCATACGCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
bub.min	ACTTCCTATTCGCATACGCAATCTTACGATCAGTTCCTAACAAACTAGGAGG	472
buba.bub	ACTTCCTATTCGCATACGCAATCTTACGATCAATTCCTAACAAACTAGGAGG	472
tra.ang	ATTTCCTGTTCGCATATGCAATCCTACGATCTATCCCCAACAAGCTAGGAGG	472
tra.eur	ACTTCCTATTCGCATATGCAATCCTACGATCAATCCCTAATAAACTAGGAGG	472
kob.ell	ACTTCTTATTCGCATATGCAATTCTACGATCAATCCCCAACAAACTAGGAGG	472
kob.meg	ATTTCTTATTCGCATACGCAATTTTACGGTCAATTCCTAATAAACTGGGAGG	472
red.aru	ACTTCTTATTTGCATATGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
red.ful	ACTTCTTATTNGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
neo.mos	ACTTTTTATTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGAGG	472
pel.cap	ATTTCCTATTTGCATATGCGATTCTACGATCAATTCCCAACAAACTAGGAGG	472
gaz.dam	ATTTCCTATTTGCATACGCAATTCTCCGATCAATTCCTAATAAACTAGGAGG	472
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mos.leu       ATTTCCTATTTGCATATGCCATTCTACGATCAATTCCCAACAAACTAGGAGG 472
mos.chr       ACTTCCTATTTGCATATGCCATCCTACGATCAATTCCCAACAAACTAGGAGG 472
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mos.leu	CGGACAATTATACCCCAGCAAACCCATTAAATACACCCCCACATATTAAACCCGAATGAT	420
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mos.ber	CGGACAATTATACCCCAGCAAACCCATTAAACACACCACCACATATTAAACCCGAATGAT	420
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bala.bor	CAGACAACTACACCCCAGCAAATCCACTCAGTACCCCAGCACACATTAAACCAGAATGAT	420
bala.edi	CAGACAACTACACTCCAGCAAATCCACTCAGTACCCCAACACACATTAAACCAGAATGAT	420
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mon.sch	ACTTCCTATTCGCCTACGCAATCCTACGATCTATCCCCAATAAACTAGGAGG	472
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sel.thi	ACTTTTTATTTGCTTACGCTATCCTACGATCCATCCCCAACAAACTAGGAGG	472
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pte.mom	ATTTCCTATTCGCATATGCTATCTTACGATCTATCCCTAACAAACTAGGCGG	472
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lor.tar	ATTTCCTATTCGCATACGCAATCCTACGATCAATCCCCAATAAACTAGGTGG	472

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homo           ATTTCCTATTCGCCTACACAATTCTCCGATCCGTCCCTAACAAACTAGGAGG 472
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cro.cro        ACTTCCTATTTGCCTATGCTATCCTGCGCTCAATCCCAAATAAACTCGGAGG 472
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ayt.ame        ACTTCCTATTCGCCTACGCCATCCTGCGATCAATCCCGAATAAACTAGGAGG 472
smi.sha        ATTTTTTATTTGCATACGCTATTCTGCGATCAATTCCAAACAAACTAGGAGG 472
vid.cha        ACTTCCTATTCGCCTACGCCATCCTACGATCCATCCCAAACAAACTAGGAGG 472
chry.pic       ACTTTCTTTTCGCTTACGCAATTCTACGATCCATCCCAAACAAATTAGGTGG 472
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BLASTN 2.1.2 [Nov-13-2000]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593689-1224-27770

Query=
(328 letters)

Database: Sequences from complete mitochondrial genomes
129 sequences; 3,164,247 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 80 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Score

```
                                                                  (bits)  Value
Sequences producing significant alignments:

ref|NC_001700.1|  Felis catus mitochondrion, complete genome          365   e-101
ref|NC_001325.1|  Phoca vitulina mitochondrion, complete genome       198   1e-51
ref|NC_002008.1|  Canis familiaris mitochondrion, complete g...       190   4e-49
ref|NC_001602.1|  Halichoerus grypus mitochondrion, complete...       180   3e-46
ref|NC_000884.1|  Cavia porcellus complete mitochondrial genome       176   5e-45
ref|NC_001808.1|  Ceratotherium simum mitochondrion, complet...       165   2e-41
ref|NC_001892.1|  Myoxus glis mitochondrion, complete genome          153   8e-38
ref|NC_001788.1|  Equus asinus mitochondrion, complete genome         151   3e-37
ref|NC_002078.1|  Orycteropus afer complete mitochondrial ge...       149   1e-36
ref|NC_001821.1|  Dasypus novemcinctus mitochondrion, comple...       141   3e-34
ref|NC_001779.1|  R.unicornis complete mitochondrial genome           135   2e-32
ref|NC_001569.1|  Mus musculus mitochondrion, complete genome         133   7e-32
ref|NC_000889.1|  Hippopotamus amphibius mitochondrion, comp...       125   2e-29
ref|NC_001640.1|  Equus caballus mitochondrion, complete genome       125   2e-29
ref|NC_001794.1|  Macropus robustus mitochondrion, complete ...       123   7e-29
ref|NC_000845.1|  Sus scrofa mitochondrion, complete genome           121   3e-28
ref|NC_001665.1|  Rattus norvegicus mitochondrial genome              121   3e-28
ref|NC_001567.1|  Bos taurus mitochondrion, complete genome           121   3e-28
ref|NC_001643.1|  Pan troglodytes mitochondrion, complete ge...       117   4e-27
ref|NC_001941.1|  Ovis aries mitochondrion, complete genome           109   1e-24
ref|NC_002391.1|  Talpa europaea mitochondrion, complete genome       103   7e-23
ref|NC_001913.1|  Oryctolagus cuniculus mitochondrion, compl...       103   7e-23
ref|NC_001644.1|  Pan paniscus mitochondrion, complete genome         101   3e-22
ref|NC_001807.2|  Human mitochondrion, complete genome                 98   4e-21
ref|NC_001601.1|  Balaenoptera musculus mitochondrion, compl...        98   4e-21
ref|NC_002009.1|  Artibeus jamaicensis mitochondrion, comple...        96   2e-20
ref|NC_001645.1|  Gorilla gorilla mitochondrion, complete ge...        92   2e-19
ref|NC_001321.1|  Balaenoptera physalus mitochondrion, compl...        90   1e-18
ref|NC_001610.1|  Didelphis virginiana mitochondrion, comple...        80   9e-16
ref|NC_002082.1|  Hylobates lar mitochondrion, complete genome         70   9e-13
ref|NC_001727.1|  Crossostoma lacustre mitochondrion, comple...        70   9e-13
ref|NC_001804.1|  Latimeria chalumnae mitochondrion, complet...        68   4e-12
ref|NC_000880.1|  Vidua chalybeata mitochondrion, complete g...        66   1e-11
ref|NC_002069.1|  Corvus frugilegus mitochondrion, complete ...        64   6e-11
ref|NC_000886.1|  Chelonia mydas mitochondrial DNA, complete...        62   2e-10
ref|NC_001646.1|  Pongo pygmaeus mitochondrion, complete genome        62   2e-10
ref|NC_001606.1|  Cyprinus carpio mitochondrion, complete ge...        62   2e-10
ref|NC_000890.1|  Mustelus manazo mitochondrion, complete ge...        60   9e-10
ref|NC_001323.1|  Gallus gallus mitochondrion, complete genome         60   9e-10
ref|NC_002079.1|  Carassius auratus mitochondrion, complete ...        58   3e-09
ref|NC_000934.1|  Loxodonta africana mitochondrion, complete...        56   1e-08
ref|NC_000878.1|  Falco peregrinus mitochondrion, complete g...        56   1e-08
ref|NC_000846.1|  Rhea americana mitochondrion, complete genome        56   1e-08
ref|NC_002196.1|  Ciconia boyciana mitochondrion, complete g...        54   5e-08
ref|NC_001960.1|  Salmo salar mitochondrion, complete genome           54   5e-08
ref|NC_001778.1|  Polypterus ornatipinnis mitochondrion, com...        54   5e-08
ref|NC_002083.1|  Pongo pygmaeus abelii mitochondrion, compl...        52   2e-07
ref|NC_001953.1|  Struthio camelus complete mitochondrial ge...        52   2e-07
ref|NC_001947.1|  Pelomedusa subrufa mitochondrion, complete...        52   2e-07
ref|NC_001770.1|  Arbacia lixula mitochondrion, complete genome        52   2e-07
```

Alignments

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                          tgaatctgaggaggctttctcagtagacaaagctaccctgacacgatttctttgcctttccac 60
cmpseq_0    1             
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NC_001325   15580  ..............a..t........t.....a...t.a...........c..a.....t  15639
NC_002008   14673     ........c...........g........a.....a.....................  14729
NC_001602   15553  ..............a..t..............a...t.a...g.......c.........  15612
NC_000884   14650  ...........g..g.................c.....a...........c.....t...  14709
NC_001808   14652  ..............a..t..c..t........c..a..t...........c..a..t...  14721
NC_001892   14654  .....t.....c........c..............t..a..c.....t.....a..t...  14713
NC_001788   14671  ...........t..a.................c.....t..c.....t............  14730
NC_002078   14663        .....c.....t.....t........a..a..a...........c.........  14716
NC_001821   14657  ................................a..t..a.....c.....c.........  14716
NC_001779   14664  ..............a........c........c.....c..c.....t............  14723
NC_001562   14625  .....t.....g....................c...t....c........c..t......  14684
NC_000892   14658  .................t..c...........c.....t.....................  14717
NC_001640   14674  ...........t..a.................c.....t..c.....c.....t......  14711
NC_001794   14670  ...........g..a.....c...........c.....c..c..c..t..c.....t..t  14727
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NC_000845 15828 ...........g.....t..c..c........a.....c...........c......... 15887
NC_001665 14610 ................................a.....a.....c.....c..a...... 14669
NC_001567 15000 ...........c..a.................a.....t..c........c..t.....t 15059
NC_001643 14655     ............a...........gcc.......t...........ca........ 14710
NC_001941 14645 ........g.....a.......................c..c.....t..c.....t... 14704
NC_002391 14671 .....t.....t..g.................g..a..c...........c......... 14730
NC_001913 14661 ..............a..t.....t..t.....c..t..t..c........c..t..t... 14720
NC_001644 14656     ............a...........gcc.......t...........ca..c..... 14711
NC_001807 15233 ................a...........gtc.c.....c............a....t... 15292
NC_001601 15096 ...........c..t..t..t..g..t.....a..a..a.....c............... 15155
NC_002009 14636 ...........t.....t..c...........a..t..c..c........c........t 14695
NC_001645 14686                                .......t............a........ 14714
NC_001321 15099 ...........c..t.....t.....t.....a..a..a.....c..t........t... 15158
NC_001610 14663 .....t........a.....c..t..t........a..a..c.....t.....t..t... 14722
NC_002082 14657    ........c....a.........t..c..c..a..c.....c..t..ca....t... 14712
NC_001727 15764 ...........g..g..............t..a...t.......g.....c......... 15823
NC_001804 14829 ..............t..t..c........c..c..a..c..g.................. 14888
NC_000880 15477      .........a.............                                 15500
NC_002069 14190       .....t..a..............cc.c..a..a..c.................. 14243
NC_000886 14718 ..............g..t...........t..a.....a..c........ca........ 14777
NC_001646 14716                                        ............a..c.t... 14736
NC_001606 15779 ...........t..g..............t..a..a..a...........c..a...... 15838
NC_000890 14841 ..............g..t...........c..c.....t.....c..t........t... 14900
NC_002079 15782 .....t..............c.....t..t..a..at.a...........c..a..t... 15841
NC_000934 14633 .................t........t.....a...t.a.at.....t..c...c....t 14692
NC_000878 14222                   ...........cc.a..a.....c........c...c.a... 14263
NC_000846 14145                   ...........cc.......a..c........c...c.g... 14186
NC_001960 15870 .....t........a..t..t........c..c.....a........t..c......... 15929
NC_001778 14763 ..............g..t.....t..t..c..a..a..t..c...........a...... 14822
NC_001953 14115      ......c..a........t.....cc.c.....a...............c.t... 14169
NC_001947 14805 ..............a..t...........t..a.....a..c........           14854
NC_001770 15069           .......t........t.....a.....a..c...........t..t... 15119

                ttcatccttccatttatcatttcagctttagcagcagtttacctcttattctttcacgag 120
tmpseq_0  61    .....t........c..t........ct......g...a......t..........t..a 15643
NC_001700 15584 ........a.....cg.ag.a.t...a...ac............a........a.....a 15699
NC_001325 15640 ........c..t..c......g...........at...a...........t..a.....a 14789
NC_002008 14730 ........a.....cg.ag.a.t...a.................a........a.....a 15672
NC_001602 15613 ..t..t........c......a.c..c....tgat..........t.......c...... 14769
NC_000884 14710 ..t.....c..c.....t..at....c.....atcac.......a..............a 14781
NC_001808 14722 ..t..t..a..c..c..t..tg....c...t.at..........t..............a 14773
NC_001892 14714 ..t..t..a..c.........a....c..g.t.atc.....t..a........c.....a 14790
NC_001788 14731 ..t.....g........t..tg.........tat.......t..a.....t..a.....a 14776
NC_002078 14717 ......t.a........t...a....a..c.t..t.........gt.......a.....a 14776
NC_001821 14717 ..t........c..c..t...ct...c.....a..c..-.....a........a.....a 14783
NC_001779 14724
                                  \
                                  |
                                  t
                ......t.a........t..g.g...c.....atc...t........c.....c.....a 14744
NC_001569 14685 ..t..t........cg.t...a....a....catc......t..a........c..t..a 14777
NC_000889 14718 ........a..c..c......a....c..g.t..tc..a..tt.a.....t........a 14793
NC_001640 14734 ..t.....a............a....c....t.ct...t..............a...... 14789
NC_001794 14730                                             ..............   14475
NC_001794 14462 ..t.....g.....c.....ta.c..c..c.....c..a..t...........g.....a 15947
NC_000845 15888 ........c.....c..t..g.c...c..t..att...a..t..t..t.....c.....a 14729
NC_001665 14670 ..t.................at....aa.t.cat..........a........c.....a 15119
NC_001567 15060 ..t...t.a..c..c......a....c...a..a..c.t..t.........t.a.....a 14770
NC_001643 14711 ..t..tt.c.....c......g....c..c.cat....t.....a..c.....c.....a 14764
NC_001941 14705 ......t.g........t..tg.g..a....t.g....t.....gt....t........a 14790
NC_002391 14731 ......t.g...........                                         14740
NC_001913 14721 ..t.....a..c..c..t...a....c...a..a..c.t..t.........t.a.....a 14771
NC_001644 14712 ......t.g..c..c..t..tg....c......a..c..............t.g.....a 15352
NC_001807 15293 .....t..c..c..c.....cat...at....atc..........a.c...........a 15215
NC_001601 15156 ..tc.a.....c..c..tg.aa.........t.at.........tt....t..a.....a 14755
NC_002009 14696 ..t.....a..c..c......a....c...a..a.cc....t........t..a.....a 14774
NC_001645 14715 ..t.....c..c..c......ct...at....att.........ca.t...........a 15218
NC_001321 15159 ..t..t........c.....t.t....a...t..t...a..t..t.....t..a...... 14782
NC_001610 14723 ........a..t..c..t...a.g..c........cc.g.....t........a...... 14772
NC_002082 14713 ...                                                          15826
NC_001727 15824                                                 ............ 15883
NC_001727 15872 ...c....g.....                                               14702
NC_001804 14887
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                                                                 .....g..c........t... 14948
NC_001804 14928                                              ..........ac......a.....a 15591
NC_000880 15567                                        ..........aacc............a 14303
NC_002069 14244 ...c....a..c...g.a...g...gc...a..cc...t.....aacc............ 14780
NC_000886 14778 ...                                                               .a 14796
NC_001646 14737 .....a..a..t..c.....ta........a..a.cc.t..................... 15841
NC_001606 15839 ...                                                                  14902
NC_000890 14901 ..                                                                   15862
NC_002079 15842 ...c....a.............                                               14708
NC_000934 14693 .....t..........                                                     14277
NC_000878 14264 ...c.a........                                         .....a.....a 14246
NC_000846 14235                                                                      14189
NC_000846 14187 ...                                                                  15932
NC_001960 15930 ...                                                                  14833
NC_001778 14823 .....t.....                                                          14184
NC_001953 14170 ...c....c......                                                      15122
NC_001770 15120 ...

                acaggatctaacaacccctcaggaatagtatccgactcagacaaaattccattccaccca 180
tmpseq_0  121   ..........................tac.....t...........c............ 15703
NC_001700 15644 ..........................tac.....t...........c...........g 15759
NC_001325 15700 ........a..........c.....ca.....................c......t.....t 14849
NC_002008 14790 ..c.....c.........t........cac...a.............................g 15732
NC_001602 15673 ........a..........c.....ca..c..................c...........t 14829
NC_000884 14770 ........a........a......c..aac..a.....c.........c............ 14841
NC_001808 14782 ........c..t.....a........ccc....a..at..........c...........t 14833
NC_001892 14774 ........g..t.....a......t..aac..a...a...........c...........g 14850
NC_001788 14791 ........c.................ccc...t...at..........c...........t 14836
NC_002078 14777 .................t.t....t..a.t..t...............c..t........g 14836
NC_001821 14777 ........a.........a....t..cccg..aa..at.....c...c...........t 14843
NC_001779 14784 .....g..c.........a.......tcc....a..at..........c.......t.....c 14804
NC_001569 14745 ........a........aa.....t..aac..a..tg....t..............c 14837
NC_000889 14778 ........c........aa.......cccc..aa..g...........c............ 14853
NC_001640 14794 ...........t..............ccc......tatg.........c...........t 14849
NC_001794 14790 ..c..t...........a..t.....caacc.........................t..... 16007
NC_000845 15948 ..c.....c........ta.c.....ccc...a...at.......................t... 14789
NC_001665 14730 ........a..t.......a.....t..aac......g..........c............c 15179
NC_001567 15120 .....c..c........aa.......tccc..a...gt..........c............c 14830
NC_001643 14771 ........a..t......cc......cacc...c....c.........a.c.........t 14824
NC_001941 14765 ........c..........a.......tcc...g...a....t.........c.......... 14814
NC_002391 14791 ........a.........a......                      ......t.....c..t.........c 14840
NC_001913 14815                                       ......t.....c..t.........c 14831
NC_001644 14772 ........a..t......cc......cacc...c....c.........a.c.........c 15412
NC_001807 15353 ..g.....a.........cc......cacc...c.t..c..t.....ca.c..........c 15275
NC_001601 15216 ........c..........a....t..ccc...t...at...t...............c 14815
NC_002009 14756 ...................a....c..tcc...a...c......t............c 14834
NC_001645 14775 ........a.........tcc...c..cccc...c.....t........ca.c.........c 15278
NC_001321 15219 ........c..........a....c..ccc.......at...t.....c............c 14842
NC_001610 14783 ........a.g...t..aa....cc...-....a.......t.......................
                                              \
                                              |
                                              a
                                                                       .........cg.c........c 14832
NC_002082 14773 ........a.....t.....t...c..cccc...c.ac..........cg.c........... 15943
NC_001727 15884 .....c..c..........g....cc..aac......g....t......cc.c.......... 14965
NC_001804 14949 ........c.........                                                  15651
NC_000880 15592 ........a.....t..aat......tcc...a....gt............................ 14363
NC_002069 14304 .....c..a.........gcc...t..tccc..a....gc.........c............. 14814
NC_001645 14797 ........a|.t......                  ........................t....... 15561
NC_001323 15531                          ..........t.....................t....... 15961
NC_002079 15939                                        ..........c.t........... 14812
NC_000934 14786                                    ..........c..c..t......... 14383
NC_000878 14363                                          ..........c.............c 14306
NC_000845 14247 ..c..g..c..........t......c.....tc....t..........c.............c 16391
NC_002195 16371                                          ..........................c 14866
NC_002083 14858                                                     ..........  14289
NC_001953 14269                                          ........c..c...........

                tactacacaatcaaagatatcctgggcctttctagtactaattcctagcactcatactactc 240
tmpseq_0  181   ..........................................................  15763
NC_001700 15704 .....t...........c.....a..t............g.tt..a.............a 15817
NC_001325 15760 .....t.....t...........a..ggcc...c.t..c..t.....tc..a.c........ 14972
NC_002008 14850 ...............g.......                                          15755
NC_001602 15733 .....t.....t.....c.....                                  ......a 15772
NC_001602 15784
```

```
NC_000884 14830 ..t..............                                                   14846
NC_001808 14842 ................c........aa..t..c.c..............ac.cgcc..a 14901
NC_001892 14834 ..t........t........t..a.....a..cc....c..tt.tccc......acc..a 14893
NC_001788 14851 ..........t.....c.....a..a.....                              14882
NC_001788 15080                                          ................    15095
NC_002078 14837 .................                                            14853
NC_001821 14837 .....t.....t...........                                      14859
NC_001779 14844 ................c.....                                       14866
NC_001569 14805 .....t.................                                      14827
NC_000889 14838 ..t...........g..c.....                                      14860
NC_001640 14854 ..t..t.....t.....c.....                                      14876
NC_001640 15085                                          ..............      15098
NC_001794 14850 ..t..t..t.........                                           14867
NC_000845 16008 ........t..t.....                                            16024
NC_001665 14790 ..t..t.....t.....                                            14806
NC_001567 15180 .....t..c..t..g..c...t......c..--........t.....t..a........a 15239
                                      \
                                      |
                                      ag
NC_001643 14831 .......................                                      14853
NC_001941 14825 ..t.....c..t.....c.....                                      14847
NC_001913 14841 .................                                            14857
NC_001644 14832 ..........c............                                      14854
NC_001807 15413 .................                                            15429
NC_001601 15276 ...........t.....                                            15292
NC_002009 14816 .....t..t..t........                                         14835
NC_001645 14835 .................c.....a.....                                14863
NC_001321 15279 ...c.......t.....                                            15295
NC_001610 14843 .....t..c..a...........                                      14865
NC_002082 14833 .....t...........c.....                                      14855
NC_001727 15944 ....                                                         15947
NC_000880 15652 ........                                                     15659
NC_002069 14364 ......t...........                                           14381
NC_001323 15562 ......t.ct.......c..t......                                  15588
NC_002079 15962 ....                                                         15965
NC_000934 14813 .....                                                        14817
NC_000878 14384 ......t.tc.............                                      14406
NC_000846 14307 ....                                                         14310
NC_002196 16392 ....t.t.cc.............a......                               16421
NC_002083 14867 .................c.....a.....                                14895
NC_001953 14290 ....                                                         14293

tmpseq_0  241   gtcctattctcaccagacctgttaggagaccccgataactacatcccctgccaaccctcta 300
NC_001700 15764 .......t...........c..........a..c...........a.........t..   15823
NC_001325 15820 ..g...........c..................a..c.....t......            15867
NC_002008 14914     ....t.....t.....a..........a..............c......a.....c... 14969
NC_001602 15793 ..a...........c.....a..g...........c.................t..c... 15852
NC_000884 14900          ....c.....a..........a..........ca..c........g..g 14949
NC_001808 14902 ..t...............a.cc..........t..c........c.........t.....  14960
NC_001892 14894 ...t........c......t.a.......................c...c........a... 14953
NC_002078 14909            ........a............                               14928
NC_000845 16071   ................ac.........a..c........c...a..a.....a...  16127
NC_001567 15240 ..a......g....c.....cc.c.........a...........c...a.....       15292
NC_001913 14901 ........t...........a..........a..c.........c.............c..t 14960
NC_001644 1484                                                 .........       1492
NC_001807 15476   ..................cc....c.....a..c..t..t.c..ta........cc..  15532
NC_002009 14880    ....t...........cc..........a..c..t..t..t..a..a..t..a..t 14935
NC_001645 14898   ..................cc..........a..c.......c.tta........c...  14954
NC_001610 14907    .............t..t..........t..c.....t..c...a..t..t..c..t 14962
NC_002082 14950                                                           ...  14952
NC_001804 15071  .......a.t...a.....................a....                    15108
NC_000885 14980               ..........a..c.....t..ca..a.............         15017
NC_002196 16454  ............ca....ac.....t......a..g.....t..c...a........    16507
NC_001960 16155                                             ...........c...    16169

tmpseq_0  301   aatacccctccccatatcaagcctgaat  328
NC_001700 15824 .................t..a.......   15851
NC_002008 14970 ..c.........a.....t..a.....    14995
NC_001602 15853 .gc.....a..a........         15872
NC_000884 14950 .....    .                     14954
NC_001892 14954 .g..............               14970
```

```
NC_001779 3081              ..............    3094
NC_000845 16128 ..c.....a........             16144
NC_001911 14961 ....................          14980
NC_001644 1493  ...c.....                     1501
NC_001807 15533 ..c...........c........c.... 15560
NC_002009 14936 .................t.....a.... 14963
NC_001645 14955 .gc.....a.....c.....          14974
NC_001610 14963 ..c.....g..t...........a.... 14990
NC_002082 14953 ..c...........c.....          14972
NC_001960 16170 gt...t..a..t................ 16197
NC_001951 14426       ..................c.... 14437
```

```
  Database: Sequences from complete mitochondrial genomes
    Posted date:  Jun 28, 2000 10:56 AM
  Number of letters in database: 3,164,247
  Number of sequences in database:  129

Lambda     K      H
    1.37    0.711     1.31

Gapped
Lambda     K      H
    1.37    0.711     1.31


Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 788
Number of Sequences: 129
Number of extensions: 788
Number of successful extensions: 168
Number of sequences better than 10.0: 77
length of query: 328
length of database: 3,164,247
effective HSP length: 15
effective length of query: 313
effective length of database: 3,162,312
effective search space: 989803656
effective search space used: 989803656
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 14 (28.2 bits)
```

Table 4

BLASTN 2.1.2 [Nov-13-2000]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer,
Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997),
"Gapped BLAST and PSI-BLAST: a new generation of protein database search
programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593400-28182-3122

Query=
(328 letters)

Database: nt
807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search
please refer to the BLAST FAQs

Taxonomy reports

Distribution of 50 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

```
                                                                 Score     E
Sequences producing significant alignments:                      (bits)  Value

gb|AY005809.1|  Panthera pardus cytochrome b gene, partial c...   603   e-170
gb|AF053054.1|AF053054  Panthera tigris sumatrae isolate Su1...   527   e-147
gb|AF053053.1|AF053053  Panthera tigris tigris isolate B7 mi...   527   e-147
gb|AF053050.1|AF053050  Panthera tigris corbetti isolate C2 ...   476   e-132
gb|AF053049.1|AF053049  Panthera tigris corbetti isolate C1 ...   476   e-132
gb|AF053025.1|AF053025  Panthera tigris tigris isolate B9 cy...   460   e-127
gb|AF053024.1|AF053024  Panthera tigris tigris isolate B8 cy...   460   e-127
gb|AF053023.1|AF053023  Panthera tigris tigris isolate B7 cy...   460   e-127
gb|AF053022.1|AF053022  Panthera tigris tigris isolate B6 cy...   460   e-127
gb|AF053021.1|AF053021  Panthera tigris tigris isolate B5 cy...   460   e-127
gb|AF053018.1|AF053018  Panthera tigris tigris isolate B2 cy...   460   e-127
gb|AF053051.1|AF053051  Panthera tigris corbetti isolate C3 ...   452   e-125
gb|AF053048.1|AF053048  Panthera tigris sumatrae isolate Su1...   452   e-125
gb|AF053047.1|AF053047  Panthera tigris sumatrae isolate Su9...   452   e-125
gb|AF053046.1|AF053046  Panthera tigris sumatrae isolate Su7...   452   e-125
gb|AF053045.1|AF053045  Panthera tigris sumatrae isolate Su6...   452   e-125
gb|AF053044.1|AF053044  Panthera tigris sumatrae isolate Su5...   452   e-125
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gb|AF053041.1|AF053041  Panthera tigris sumatrae isolate Su2...   452   e-125
gb|AF053040.1|AF053040  Panthera tigris sumatrae isolate Su1...   452   e-125
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gb|AF053038.1|AF053038  Panthera tigris altaica isolate S14 ...   452   e-125
gb|AF053037.1|AF053037  Panthera tigris altaica isolate S13 ...   452   e-125
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gb|AF053035.1|AF053035  Panthera tigris altaica isolate S11 ...   452   e-125
gb|AF053034.1|AF053034  Panthera tigris altaica isolate S10 ...   452   e-125
gb|AF053033.1|AF053033  Panthera tigris altaica isolate S8 c...   452   e-125
gb|AF053032.1|AF053032  Panthera tigris altaica isolate S7 c...   452   e-125
gb|AF053031.1|AF053031  Panthera tigris altaica isolate S6 c...   452   e-125
gb|AF053030.1|AF053030  Panthera tigris altaica isolate S5 c...   452   e-125
gb|AF053029.1|AF053029  Panthera tigris altaica isolate S4 c...   452   e-125
gb|AF053028.1|AF053028  Panthera tigris altaica isolate S3 c...   452   e-125
gb|AF053027.1|AF053027  Panthera tigris altaica isolate S2 c...   452   e-125
gb|AF053026.1|AF053026  Panthera tigris altaica isolate S1 c...   452   e-125
gb|AF053020.1|AF053020  Panthera tigris tigris isolate B4 cy...   452   e-125
gb|AF053019.1|AF053019  Panthera tigris tigris isolate B3 cy...   452   e-125
gb|AF053043.1|AF053043  Panthera tigris sumatrae isolate Su4...   444   e-122
emb|X82301.1|MIPTCYTB  P.tigris mitochondrial cytochrome b gene   444   e-122
gb|AF053052.1|AF053052  Panthera leo cytochrome b (cytb) gen...   440   e-121
emb|X82300.1|MIPLCYTBG  P.leo mitochondrial cytochrome b gene     438   e-121
dbj|AB004238.1|AB004238  Felis catus mitochondrial DNA for c...   399   e-106
dbj|AB004237.1|AB004237  Felis catus mitochondrial DNA for c...   381   e-103
emb|X82296.1|MIFDCYTB  F.domesticus mitochondrial cytochrome...   377   e-102
ref|NC_001700.1|  Felis catus mitochondrion, complete genome      365   1e-98
gb|U20753.1|FCU20753  Felis catus mitochondrion, complete ge...   365   1e-98
gb|AF125145.1|AF125145  Viverricula indica cytochrome b gene...   276   7e-72
gb|AF125144.1|AF125144  Chrotogale owstoni cytochrome b gene...   270   4e-70
gb|AF154975.1|AF154975  Martes martes specimen_voucher AF175...   256   7e-66
dbj|AB051237.1|AB051237  Martes martes mitochondrial cytb ge...   256   7e-66
gb|AF125149.1|AF125149  Viverra tangalunga cytochrome b gene...   246   6e-63
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Alignments

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AF053018  487  ...........g..t............................................. 546
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AF053048  487  ...........g..t............................................. 546
AF053047  487  ...........g..t.............................................
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AF053019    487    ...........g..t.............................................  546
AF053043    487    ...........g..t.............................................  546
X82301      487    ...........g..t.............................................  546
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X82300      490       ............................c............................  546
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AB004237    487    ...........g...................c.....a...............t......  546
X82296      487    ...........g...................c.....a..............g.......  546
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AF154975    487    ..............g.....g..........c.....a..g.........c.........  546
AB051237    487    ..............g.....g..........c.....a..g.........c.........  546
AF125149    357    ...........g.....t..........g..c...t.a...............t......  416

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X82300     667    ......t................a..............t...t..a.............. 726
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AB004237   667    ......t...........c....a..t.............g.tt.a.............. 726
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AB051237   667    .........c........c....a...gcc...t.c..........tg......a....a 726
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AF053042   727    ....................a...........t..............c........c... 786
AF053041   727    ....................a...........t..............c........c... 786
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AF053020    727    ....................a...........t..............c........c... 786
AF053019    727    ....................a...........t..............c........c... 786
AF053043    727    ....................a...........t..............c........c... 786
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AF053052    727    ....................a........t.....c.....t.c...c.....t...... 786
X82300      727    ....................a........t.....c.....t.c...c.....t...... 786
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X82296      727    .....r..t............c..........a..c...........a.........t.. 786
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AF125144    597    ..t.....t.....t.....t...........a..c.......c......a......... 656
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AB051237    727    ..a...........c.....c.g.........a..c...........c........a..c 786
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AF053022    787    .................t.....c.... 814
AF053021    787    .................t.....c.... 814
AF053018    787    .................t.....c.... 814
AF053051    787    .................t.....c.... 814
AF053048    787    .................t.....c.... 814
AF053047    787    .................t.....c.... 814
AF053046    787    .................t.....c.... 814
AF053045    787    .................t.....c.... 814
AF053044    787    .................t.....c.... 814
AF053042    787    .................t.....c.... 814
AF053041    787    .................t.....c.... 814
AF053040    787    .................t.....c.... 814
AF053039    787    .................t.....c.... 814
AF053038    787    .................t.....c.... 814
AF053037    787    .................t.....c.... 814
AF053036    787    .................t.....c.... 814
AF053035    787    .................t.....c.... 814
AF053034    787    .................t.....c.... 814
AF053033    787    .................t.....c.... 814
AF053032    787    .................t.....c.... 814
AF053031    787    .................t.....c.... 814
AF053030    787    .................t.....c.... 814
AF053029    787    .................t.....c.... 814
AF053028    787    .................t.....c.... 814
AF053027    787    .................t.....c.... 814
AF053026    787    .................t.....c.... 814
AF053020    787    .................t.....c.... 814
AF053019    787    .................t.....c.... 814
AF053043    787    .................t.....c.... 814
X82301      787    .................t.....c.... 814
```

```
AF051052   787   .gc..................a.....    812
X82100     787   .gc..................a.......  814
AB004238   787   ................t..a.......    814
AB004237   787   ................t..a.......    814
X82296     787   ................t..a.......    814
NC_001700  15824 ................t..a.......    15851
U20753     15824 ................t..a.......    15851
AF125144   657   ..c.....                       664
AF154975   787   ..c..a..a.......               803
AB051237   787   ..c..a..a.......               803
AF125149   657   ..c.....                       664
```

```
  Database: nt
    Posted date:  Mar 2, 2001 12:20 AM
  Number of letters in database: 2,863,827,885
  Number of sequences in database:  807,597

Lambda     K      H
    1.37    0.711     1.31

Gapped
Lambda     K      H
    1.37    0.711     1.31


Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 460542
Number of Sequences: 807597
Number of extensions: 460542
Number of successful extensions: 22671
Number of sequences better than 10.0: 6487
length of query: 328
length of database: 2,863,827,885
effective HSP length: 20
effective length of query: 308
effective length of database: 2,847,675,945
effective search space: 877084191060
effective search space used: 877084191060
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 19 (38.2 bits)
```

Table 5. Reference animals and the allocated code numbers included in the study

SN.	Code number	Name of the animal	Zoological name
1	bhz25t	Indian tiger	*Panthera tigris tigris*
2	bhz26t	Indian tiger	*Panthera tigris tigris*
3	bhz30t	Indian tiger	*Panthera tigris tigris*
4	bhz45t	Indian tiger	*Panthera tigris tigris*
5	bhz56t	Indian tiger	*Panthera tigris tigris*
6	bhz63t	Indian tiger	*Panthera tigris tigris*
7	bhz20wt	Indian white tiger	*Panthera tigris bengalensis*
8	bhz22wt	Indian white tiger	*Panthera tigris bengalensis*
9	bhz23wt	Indian white tiger	*Panthera tigris bengalensis*
10	bhz28wt	Indian white tiger	*Panthera tigris bengalensis*
11	gz1l	Normal leopard	*Panthera pardus*
12	gz2l	Normal leopard	*Panthera pardus*
13	gz3l	Normal leopard	*Panthera pardus*
14	gz21cl	Clouded leopard	*Neofelis nebulosa*
15	gz22cl	Clouded leopard	*Neofelis nebulosa*
16	darz14sl	Snow leopard	*Panthera unicia*
17	darz15sl	Snow leopard	*Panthera unicia*
18	darz16sl	Snow leopard	*Panthera unicia*
19	sbz22al	Asiatic lion	*Panthera leo persica*
20	sbz38al	Asiatic lion	*Panthera leo persica*
21	sbz39al	Asiatic lion	*Panthera leo persica*
22	humsk	Human	*Homo sapiens sapiens*
23	chimss	Chimpanzee	*Pan sp.*

Table 6. Multiple sequence alignments of the cytochrome b sequences of reference animals with the sequence obtained from confiscated animal remain

```
sbz22al       TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 50
sbz38al       TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
sbz39al       TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
adil.flesh    TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACACGATTCTTTGCCTTCCAC 60
gz1nl         TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC 60
gz2nl         TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC 60
gz3nl         TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACACGATTCTTTGCCTTCCAC 60
bhz23wt       TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz28wt       TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz22wt       TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz20wt       TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz63t        TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz56t        TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz26t        TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz30t        TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz45t        TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
bhz25t        TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
dz14sl        TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
dz15sl        TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
dz16sl        TGAATCTGAGGAGGCTTCTCAGTACACAAAGCCACCCTGACACGATTCTTTGCCTTCCAC 60
gz21cl        TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTTTTCGCCTTCCAC 60
gz22cl        TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCCACCCTGACACGATTTTTCGCCTTCCAC 60
chimss        TGAATCTGAGGAGGCTACTCAGTAGACAGCCCTACCCTTACACGATTCTTCACCTTCCAC 60
humsk         TGAATCTGAGGAGGCTACTCAGTAGACAGTCCCACCCTCACACGATTCTTTACCTTTCAC 60
              **************** ******* ***   * *** * ******** **  **** ***

sbz22al       TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA 120
sbz38al       TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA 120
sbz39al       TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTGTTCCTCCATGAA 120
adil.flesh    TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG 120
gz1nl         TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG 120
gz2nl         TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG 120
gz3nl         TTCATCCTTCCATTTATCATCTCAGCTCTAGCAGCAGTCCACCTCCTATTCCTTCACGAG 120
bhz23wt       TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz28wt       TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz22wt       TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz20wt       TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz63t        TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz56t        TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz26t        TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz30t        TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz45t        TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
bhz25t        TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
dz14sl        TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
dz15sl        TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 120
dz16sl        TTCATCCTTCCATTTATCATCTCAGCCCTAGCAGCAGTCCACCTCCTATTCCTCCATGAG 129
gz21cl        TTCATCCTCCCATTTATCATCTCAGCCTTAGCAGCAGTTCACCTTCTATTTCTCCATGAA 120
gz22cl        TTCATCCTCCCATTTATCATCTCAGCCTTAGCAGCAGTTCACCTTCTATTTCTCCATGAA 120
chimss        TTTATCTTACCCTTCATTATCACAGCCCTAACAACACTTCATCTCCTATTCTTACACGAA 120
humsk         TTCATCTTGCCCTTCATTATTGCAGCCCTAGCAGCACTCCACCTCCTATTCTTGCACGAA 120
              ** *** * ** ** ** **  **** ** ** ** * ** ** ** **  * ** **

sbz22al       ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAATTCCATTCCATCCA 180
sbz38al       ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAATTCCATTCCATCCA 180
```

```
sbz39al      ACAGGATCTAATAACCCCTCAGGAATGGTATCTGACTCAGATAAAATTCCATTCCATCCA 180
adil.flesh   ACAGGATCTAACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA 180
gz1nl        ACAGGATCTAACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCATTCCACCCA 180
gz2nl        ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCATTCCACCCA 180
gz3nl        ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATTCCATTCCACCCA 180
bhz23wt      ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz28wt      ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz22wt      ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz20wt      ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz63t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz56t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz26t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz30t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz45t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
bhz25t       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
dz14sl       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
dz15sl       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
dz16sl       ACAGGATCTAACAACCCCTCAGGAATAGTATCTGACTCAGACAAAATCCCGTTCCACCCA 180
gz21cl       ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTCAGACAAAATCCCGTTCCACCCG 180
gz22cl       ACAGGATCCAATAACCCCTCAGGAATGGTATCCGATTCAGACAAAATCCCGTTCCACCCG 180
chimss       ACAGGATCAAATAACCCCCTGGGAATCACCTCCCACTCCGACAAAATTACCTTCCACCCC 180
humsk        ACGGGATCAAACAACCCCCTAGGAATCACCTCCCATTCCGATAAAATCATCTTCCACCCT 180
             ** ***** ** ******    *****    **  * ** ** *****    ***** **

sbz22al      TACTATACAATCAAAGATATCCTAGGCCTTCTAGTACTAATCTTAACACTCATACTACTC 240
sbz38al      TACTATACAATCAAAGATATCCTAGGCCTTCTAGTACTAATCTTAACACTCATACTACTC 240
sbz39al      TACTATACAATCAAAGATATCCTAGGCCTTCTAGTACTAATCTTAACACTCATACTACTC 240
adil.flesh   TACTACACAATCAAAGATATCCTGGGCCTTCTAGTACTAATCCTAGCACTCATACTACTC 240
gz1nl        TACTACACAATCAAAGATATCCTGGGCCTTCTAGTACTAATCCTAGCACTCATACTACTC 240
gz2nl        TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCTTAGCACTCATACTACTC 240
gz3nl        TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCTTAGCACTCATACTACTC 240
bhz23wt      TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz28wt      TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz22wt      TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz20wt      TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz63t       TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz56t       TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz26t       TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz30t       TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz45t       TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
bhz25t       TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
dz14sl       TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
dz15sl       TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
dz16sl       TACTACACAATCAAAGACATCCTGGGCCTTCTAGTACTAATCCTAACACTCATACTACTC 240
gz21cl       TACTATACAATCAAAGATATCCTAGGCCTCCTAGTTCTAATTCTAGCGCTCACACTACTT 240
gz22cl       TACTATACAATCAAAGATATCCTAGGCCTCCTAGTTCTAATTCTAGCGCTCACACTACTT 240
chimss       TACTACACAATCAAAGATATCCTTGGCTTATTCCTTTTCCTCCTTATCCTAATGACATTA 240
humsk        TACTACACAATCAAAGACGCCCTCGGCTTACTTCTCTTCCTTCTCTCCTTAATGACATTA 240
             ***** ***********    *** *** *  *  *  *  *  *        * *    * *

sbz22al      GTCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACTATACCCCCGCCAATCCTCTA 300
sbz38al      GTCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACTATACCCCCGCCAATCCTCTA 300
sbz39al      GTCCTATTCTCACCAGACCTATTAGGAGATCCCGACAACTATACCCCCGCCAATCCTCTA 300
adil.flesh   GTCCTATTCTCACCAGACCTGTTAGGAGACCCCGATAACTACATCCCTGCCAACCCTCTA 300
gz1nl        GTCCTATTCTCACCAGACCTGTTAGGAGACCCCGATAACTACATCCCTGCCAACCCTCTA 300
gz2nl        GTCCTATTCTCACCAGACCTGTTGGGAGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
gz3nl        GTCCTATTCTCACCAGACCTGTTGGGAGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz23wt      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
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bhz28wt      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz22wt      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz20wt      GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz63t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz56t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz26t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz30t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz45t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
bhz25t       GTCCTATTCTCACCAGACCTATTAGGGGACCCCGATAACTACATCCCCGCCAACCCTCTA 300
dz14sl       GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCTCTA 300
dz15sl       GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCTCTA 300
dz16sl       GTCCTATTCTCACCAGACCTATTAGGGGACGCCGATAACTACATCCCCGCCAACCCTCTA 300
gz21cl       GTTCTATTCTCCCCAGACCTACTAGGAGACCCTGACAATTACACTCCCGCCAACCCTCTA 300
gz22cl       GTTCTATTCTCCCCAGACCTACTAGGAGACCCTGACAATTACACTCCCGCCAACCCTCTA 300
chimss       ACACTATTCTCACCAGACCTCCTGGGCGATCCAGACAACTATACCCTAGCTAACCCCCTA 300
humsk        ACACTATTCTCACCAGACCTCCTAGGCGACCCAGACAATTATACCCTAGCCAACCCCTTA 300
                 ******** ********  * ** **  * ** ** ** *  *  ** ** **  **

sbz22al      AGCACCCCTCCCCATATCAAACCTGAAT 328
sbz38al      AGCACCCCTCCCCATATCAAACCTGAAT 328
sbz39al      AGCACCCCTCCCCATATCAAACCTGAAT 328
adil.flesh   AATACCCCTCCCCATATCAAGCCTGAAT 328
gz1nl        AATACCCCTCCCCATATCAAGCCTGAAT 328
gz2nl        AATACCCCTCCCCATATCAAGCCTGAAT 328
gz3nl        AATACCCCTCCCCATATCAAGCCTGAAT 328
bhz23wt      AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz28wt      AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz22wt      AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz20wt      AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz63t       AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz56t       AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz26t       AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz30t       AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz45t       AACACCCCTCCCCATATCAAGCGCGAAT 328
bhz25t       AACACCCCTCCCCATATCAAGCGCGAAT 328
dz14sl       AACACCCCTCCCCATATCAAGCCCGAAT 328
dz15sl       AACACCCCTCCCCATATCAAGCCCGAAT 328
dz16sl       AACACCCCTCCCCATATCAAGCCCGAAT 328
gz21cl       AATACCCCTCCCCATATCAAGCCTGAAT 328
gz22cl       AATACCCCTCCCCATATCAAGCCTGAAT 328
chimss       AACACCCCACCCCACATTAAACCCGAAT 328
humsk        AACACCCCTCCCCACATCAAGCCCGAAT 328
             *  ***** ***** ** ** *  ****
```

Table 7a

Position	17	25	29	30	31	33	37	39	48	51	52	57	63	67	69	72	75	78	81	82	87	88	91	94	97	99	102	105	108	111	112
adil.flesh	T	G	A	A	G	T	C	G	C	T	G	C	C	C	T	A	T	C	C	T	T	C	G	G	G	C	C	C	A	C	C
gz1l	.	.	.	.	.	.	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
[redacted]																															
bhz25t	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.
bhz26t	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.
bhz30t	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.
bhz45t	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.
bhz56t	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.
bhz20wt	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.
bhz22wt	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.
bhz23wt	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.
dz14sl	[illegible]	C	[illegible]	[illegible]	[illegible]	C	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	C	[illegible]	.	.	.	.	.	.	.	.	.
dz15sl	[illegible]	C	[illegible]	[illegible]	[illegible]	C	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	C	[illegible]	.	.	.	.	.	.	.	.	.
sbz22al	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	G	.	.
sbz38al	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	G	.	.
gz21cl	.	.	.	.	.	C	.	.	T	C	.	.	.	.	C	.	.	.	.	.	C	T	.	.	.	T	.	T	.	T	.
gz22cl	.	.	.	.	.	C	.	.	T	C	.	.	.	.	C	.	.	.	.	.	C	T	.	.	.	T	.	T	.	T	.
chimss	A	[illegible]	G	C	C	[illegible]	[illegible]	T	[illegible]	C	A	[illegible]	T	T	A	C	C	T	[illegible]	A	C	[illegible]	A	A	C	T	T	[illegible]	[illegible]	[illegible]	T
humsk	A	[illegible]	G	T	C	C	[illegible]	C	[illegible]	[illegible]	A	T	[illegible]	T	G	C	C	T	T	G	C	[illegible]	[illegible]	[illegible]	C	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	T

Table 7b

Position	114	117	120	123	129	132	139	140	141	147	148	149	150	153	154	156	159	162	168	169	170	171	177	180	186	198	199	200	204	208	210
adll.flesh	T	C	G	A	T	C	T	C	A	A	G	T	A	C	G	C	A	C	T	C	C	A	C	A	C	T	A	T	G	C	T
gz1l	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
bhz25t	C	T	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	.	C	.	.	G	.	.	.	C	.	.	.	.	.
bhz26t	C	T	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	.	C	.	.	G	.	.	.	C	.	.	.	.	.
bhz30t	C	T	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	.	C	.	.	G	.	.	.	C	.	.	.	.	.
bhz45t	C	T	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	.	C	.	.	G	.	.	.	C	.	.	.	.	.
bhz56t	C	T	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	.	C	.	.	G	.	.	.	C	.	.	.	.	.
bhz20wt	C	T	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	.	C	.	.	G	.	.	.	C	.	.	.	.	.
bhz22wt	C	T	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	.	C	.	.	G	.	.	.	C	.	.	.	.	.
bhz23wt	C	T	.	.	.	.	.	.	.	.	.	.	.	T	.	.	.	.	C	.	.	G	.	.	.	C	.	.	.	.	.
dz14sl [illegible]	C	T	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	T	[illegible]	[illegible]	[illegible]	[illegible]	C	.	.	G	.	.	.	C	.	.	.	.	.
dz15sl [illegible]	C	T	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	T	[illegible]	[illegible]	[illegible]	[illegible]	C	[illegible]	[illegible]	G	[illegible]	[illegible]	.	C	.	.	[illegible]	[illegible]	[illegible]
sbz22al	C	T	A	.	.	T	.	.	.	G	.	.	.	T	.	.	.	T	.	.	.	.	T	.	T	.	.	.	A	.	.
sbz38al	C	T	A	.	.	T	.	.	.	G	.	.	.	T	.	.	.	T	.	.	.	.	T	.	T	.	.	.	A	.	.
gz21cl	C	T	A	.	C	T	.	.	.	G	.	.	.	.	.	T	.	.	C	.	.	G	.	G	T	.	.	.	A	.	C
gz22cl	C	T	A	.	C	T	.	.	.	G	.	.	.	.	.	T	.	.	C	.	.	G	.	G	T	.	.	.	A	.	C
chimss	[A]	[illegible]	[A]	[illegible]	[A]	[T]	[C]	[T]	[G]	[C]	[A]	[C]	[C]	[illegible]	[C]	[illegible]	[C]	[illegible]	[illegible]	[A]	[illegible]	[C]	[illegible]	[C]	[illegible]	[illegible]	[illegible]	[illegible]	[T]	[illegible]	[A]
humsk	[G]	[illegible]	[A]	[G]	[A]	[illegible]	[C]	[T]	[illegible]	[C]	[A]	[C]	[C]	[illegible]	[C]	[T]	[C]	[T]	[C]	[A]	[T]	[C]	[illegible]	[T]	[illegible]	[C]	[G]	[C]	[C]	[T]	[A]

Table 7c

Position	211	213	214	216	217	219	220	222	223	225	226	227	228	229	231	233	234	235	236	238	240	241	242	243	252	261	262	264	267	270	271
adll.flesh	C	A	G	A	C	A	A	C	C	A	G	C	A	C	C	T	A	C	T	C	C	G	T	C	A	G	T	A	A	C	C
gz1l	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
bhz25t	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	G	.	.
bhz26t	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	G	.	.
bhz30t	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	G	.	.
bhz45t	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	G	.	.
bhz56t	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	G	.	.
bhz20wt	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	G	.	.
bhz22wt	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	G	.	.
bhz23wt	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	G	.	.
dz14sl	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	A	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	.	.	.	A	.	.	G	.	G
dz15sl	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	A	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	.	.	.	A	.	.	G	.	G
sbz22al	.	.	.	.	.	.	.	.	T	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	T	.
sbz38al	.	.	.	.	.	.	.	.	T	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	T	.
gz21cl	.	.	.	T	.	.	.	T	.	.	.	.	G	.	.	C	.	.	.	.	T	.	.	T	C	A	C	.	.	.	.
gz22cl	.	.	.	T	.	.	.	T	.	.	.	.	G	.	.	C	.	.	.	.	T	.	.	T	C	A	C	.	.	.	.
chlmss	T	C	C	T	T	C	C	[illegible]	[illegible]	T	A	T	C	[illegible]	A	[illegible]	G	A	C	T	A	A	C	A	[illegible]	C	C	G	C	T	[illegible]
humsk	[illegible]	T	C	C	T	C	C	T	[illegible]	C	T	[illegible]	C	T	A	[illegible]	G	A	C	T	A	A	C	A	[illegible]	C	C	[illegible]	C	[illegible]	[illegible]

Table 7d

Position	273	276	279	282	284	285	287	288	291	294	297	298	302	303	309	315	318	321	323	324
adll.flesh	C	T	C	C	T	C	C	T	C	C	T	C	A	T	T	T	C	G	C	T
gz1l	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.
gz22l	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	.	G	[illegible]	[illegible]	[illegible]	[illegible]	.	[illegible]	[illegible]	.	.	[illegible]	[illegible]	[illegible]
gz23l	[illegible]	[illegible]	[illegible]	[illegible]	.	[illegible]	.	G	[illegible]	[illegible]	.	[illegible]	[illegible]	.	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
bhz25t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz26t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz30t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz45t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz56t	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz20wt	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz22wt	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
bhz23wt	.	.	.	.	.	.	.	C	.	.	.	.	.	C	.	.	.	.	G	C
dz14sl	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	C	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	C	[illegible]	[illegible]	[illegible]	[illegible]	.	C
dz15sl	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	C	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	C	[illegible]	[illegible]	[illegible]	.	.	C
sbz22al	.	C	.	T	C	.	.	C	.	T	.	.	G	C	.	.	.	A	.	.
sbz38al	.	C	.	T	C	.	.	C	.	T	.	.	G	C	.	.	.	A	.	.
gz21cl	T	C	T	.	C	T	.	C	.	.	.	.	.	.	.	.	.	.	.	.
gz22cl	T	C	T	.	C	T	.	C	.	.	.	.	.	.	.	.	.	.	.	.
chlmss	A	C	[illegible]	T	C	[illegible]	T	A	T	[illegible]	C	[illegible]	[illegible]	C	A	C	T	A	[illegible]	C
humsk	A	C	T	T	C	[illegible]	T	A	[illegible]	[illegible]	C	T	[illegible]	C	[illegible]	C	[illegible]	[illegible]	[illegible]	C

Table 8. Percent similarity matrix calculated by pair-vise comparisons of cytochrome b gene sequences revealed from 'adil.flesh' and different felids

	bhz20wt	bhz25t	dz14sl	humsk	chlmss	sbz22al	gz1L	gz2L	gz3L	gz21cl	adil.flesh
bhz20wt		100	99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
bhz25t	100		99.1	81.7	78.7	93.3	95.1	95.4	95.4	89.6	95.4
dz14sl	99.1	99.1		81.4	78.4	93	94.8	95.1	95.1	89.3	95.1
humsk	81.7	81.7	81.4		86.9	79.6	81.1	80.2	80.2	79	81.4
chlmss	78.7	78.7	78.4	86.9		78.7	79.6	78.7	78.7	76.8	79.9
sbz22al	93.3	93.3	93	79.6	78.7		92.1	92.4	92.4	89	92.4
gz1L	95.1	95.1	94.8	81.1	79.6	92.1		98.5	98.5	89.3	99.7
gz2L	95.4	95.4	95.1	80.2	78.7	92.4	98.5		100	88.1	98.2
gz3L	95.4	95.4	95.1	80.2	78.7	92.4	98.5	100		88.1	98.2
gz21cl	89.6	89.6	89.3	79	76.8	89	89.3	88.1	88.1		89.6
adil.flesh	95.4	95.4	95.1	81.4	79.9	92.4	99.7	98.2	98.2	89.6	

Table 10

BLASTN 2.1.2 [Nov-13-2000]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984591695-10075-13605

Query=
(25 letters)

Database: nt
807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Sequences producing significant alignments:		Score (bits)	E Value
gb|AF231651.1|AF231651	Strongylura notata clone HB-82 cytoc...	50	2e-05
gb|AF231650.1|AF231650	Strongylura notata clone HB-159 cyto...	50	2e-05
ref|NC_002672.1|	Dinornis giganteus mitochondrion, complete...	50	2e-05
ref|NC_002673.1|	Emeus crassus mitochondrion, complete genome	50	2e-05
gb|AF232015.1|AF232015	Nothrotheriops shastensis cytochrome...	50	2e-05
gb|AF232013.1|AF232013	Bradypus variegatus cytochrome b gen...	50	2e-05
gb|AY016015.1|	Emeus crassus mitochondrion, complete genome	50	2e-05
gb|AY016013.1|	Dinornis giganteus mitochondrion, complete g...	50	2e-05
gb|AY016014.1|	Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb|AF230167.1|AF230167	Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05
gb|AF074594.1|AF074594	Baeolophus bicolor cytochrome b gene...	50	2e-05
gb|AY005210.1|	Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb|AY005209.1|	Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb|AY005208.1|	Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb|AY005205.1|	Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb|AY005204.1|	Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb|AY005203.1|	Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05
gb|AY005201.1|	Poospiza boliviana cytochrome b (cytb) gene,...	50	2e-05
gb|AY005199.1|	Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb|AY005198.1|	Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb|AF155870.1|AF155870	Heterocephalus glaber cytochrome b (...	50	2e-05
gb|AF189123.1|AF189123	Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb|AF102099.1|AF102099	Criniferoides leucogaster cytochrome...	50	2e-05
gb|AF102095.1|AF102095S1	Corythaixoides concolor cytochrome...	50	2e-05
gb|AF271065.1|AF271065	Mustela erminea specimen-voucher AF1...	50	2e-05
gb|AF243857.1|AF243857	Strongylura notata notata cytochrome...	50	2e-05
gb|AF243856.1|AF243856	Strongylura notata forsythia cytochr...	50	2e-05
ref|NC_001567.1|	Bos taurus mitochondrion, complete genome	50	2e-05
gb|AF306872.1|AF306872	Brachyramphus marmoratus haplotype M...	50	2e-05
gb|AF306871.1|AF306871	Brachyramphus marmoratus haplotype M...	50	2e-05
gb|AF306870.1|AF306870	Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF306869.1|AF306869	Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF306868.1|AF306868	Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF010406.1|AF010406	Ovis aries complete mitochondrial ge...	50	2e-05
gb|AF248662.1|AF248662	Gryllus campestris haplotype 2 cytoc...	50	2e-05
gb|AF248661.1|AF248661	Gryllus campestris haplotype 1 cytoc...	50	2e-05
gb|AF096462.1|AF096462	Rhipidura albicollis cytochrome b ge...	50	2e-05
gb|AF283644.1|AF283644	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283643.1|AF283643	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283642.1|AF283642	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283641.1|AF283641	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283640.1|AF283640	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283639.1|AF283639	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283637.1|AF283637	Elaphe obsoleta LSUMZ 45359 cytochro...	50	2e-05
gb|AF283636.1|AF283636	Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05
gb|AF283635.1|AF283635	Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05
gb|AF283634.1|AF283634	Elaphe obsoleta LSUMZ 44335 cytochro...	50	2e-05
gb|AF283633.1|AF283633	Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05
gb|AF283632.1|AF283632	Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05
gb|AF283631.1|AF283631	Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05
gb|AF283630.1|AF283630	Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05
gb|AF283629.1|AF283629	Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05
gb|AF283628.1|AF283628	Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05
gb|AF283627.1|AF283627	Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05
gb|AF283626.1|AF283626	Elaphe obsoleta LSUMZ 40943 cytochro...	50	2e-05
gb|AF283625.1|AF283625	Elaphe obsoleta LSUMZ 37499 cytochro...	50	2e-05
gb|AF283624.1|AF283624	Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05
gb|AF283623.1|AF283623	Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05
gb|AF283622.1|AF283622	Elaphe obsoleta LSUMZ 40444 cytochro...	50	2e-05
gb|AF283621.1|AF283621	Elaphe obsoleta LSUMZ 39925 cytochro...	50	2e-05
gb|AF283620.1|AF283620	Elaphe obsoleta LSUMZ 39163 cytochro...	50	2e-05
gb|AF283619.1|AF283619	Elaphe obsoleta LSUMZ39162 cytochrom...	50	2e-05
gb|AF283618.1|AF283618	Elaphe obsoleta LSUMZ H15896 cytochr...	50	2e-05
gb|AF283617.1|AF283617	Elaphe obsoleta LSUMZ H15892 cytochr...	50	2e-05
gb|AF283616.1|AF283616	Elaphe obsoleta LSUMZ 15891 cytochro...	50	2e-05
gb|AF283615.1|AF283615	Elaphe obsoleta LSUMZ H15890 cytochr...	50	2e-05
gb|AF283614.1|AF283614	Elaphe obsoleta LSUMZ H15887 cytochr...	50	2e-05
gb|AF283613.1|AF283613	Elaphe obsoleta LSUMZ H15884 cytochr...	50	2e-05

Table 9. Animals selected for validation of minimum P'S score for efficient amplification of DNA templates in PCR

SL.	Name	P, S/AFF	P, S/AFR
1	Indian black buck (Antilope cervicapra)	97, 58	96, 54
2	Sheep (Ovis	87, 53	96, 54
3	Pig (*Sus scrofa*)	87, 52	87, 41
4	Fresh water dolphin (*Platanista gangetica*)	86, 49	82, 47

Sequences producing significant alignments:	Score (bits)	E Value
gb|AF231651.1|AF231651 Strongylura notata clone HB-82 cytoc...	50	2e-05
gb|AF231650.1|AF231650 Strongylura notata clone HB-159 cyto...	50	2e-05
ref|NC_002672.1| Dinornis giganteus mitochondrion, complete...	50	2e-05
ref|NC_002673.1| Emeus crassus mitochondrion, complete genome	50	2e-05
gb|AF232015.1|AF232015 Nothrotheriops shastensis cytochrome...	50	2e-05
gb|AF232013.1|AF232013 Bradypus variegatus cytochrome b gen...	50	2e-05
gb|AY016015.1| Emeus crassus mitochondrion, complete genome	50	2e-05
gb|AY016013.1| Dinornis giganteus mitochondrion, complete g...	50	2e-05
gb|AY016014.1| Dromaius novaehollandiae mitochondrion, part...	50	2e-05
gb|AF230167.1|AF230167 Bonasa umbellus cytochrome b (CYTB) ...	50	2e-05
gb|AF074594.1|AF074594 Baeolophus bicolor cytochrome b gene...	50	2e-05
gb|AY005210.1| Poospiza melanoleuca isolate 3 cytochrome b ...	50	2e-05
gb|AY005209.1| Poospiza melanoleuca isolate 2 cytochrome b ...	50	2e-05
gb|AY005208.1| Poospiza melanoleuca isolate 1 cytochrome b ...	50	2e-05
gb|AY005205.1| Poospiza hispaniolensis cytochrome b (cytb) ...	50	2e-05
gb|AY005204.1| Poospiza garleppi cytochrome b (cytb) gene, ...	50	2e-05
gb|AY005203.1| Poospiza erythrophrys cytochrome b (cytb) ge...	50	2e-05
gb|AY005201.1| Poospiza boliviana cytochrome b (cytb) gene,...	50	2e-05
gb|AY005199.1| Poospiza alticola isolate 2 cytochrome b (cy...	50	2e-05
gb|AY005198.1| Poospiza alticola isolate 1 cytochrome b (cy...	50	2e-05
gb|AF155870.1|AF155870 Heterocephalus glaber cytochrome b (...	50	2e-05
gb|AF189123.1|AF189123 Glyptotermes eukalypti cytochrome b ...	50	2e-05
gb|AF102099.1|AF102099 Criniferoides leucogaster cytochrome...	50	2e-05
gb|AF102095.1|AF102095S1 Corythaixoides concolor cytochrome...	50	2e-05
gb|AF271065.1|AF271065 Mustela erminea specimen-voucher AF1...	50	2e-05
gb|AF243857.1|AF243857 Strongylura notata notata cytochrome...	50	2e-05
gb|AF243856.1|AF243856 Strongylura notata forsythia cytochr...	50	2e-05
ref|NC_001567.1| Bos taurus mitochondrion, complete genome	50	2e-05
gb|AF306872.1|AF306872 Brachyramphus marmoratus haplotype M...	50	2e-05
gb|AF306871.1|AF306871 Brachyramphus marmoratus haplotype M...	50	2e-05
gb|AF306870.1|AF306870 Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF306869.1|AF306869 Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF306868.1|AF306868 Brachyramphus brevirostris haplotype...	50	2e-05
gb|AF010406.1|AF010406 Ovis aries complete mitochondrial ge...	50	2e-05
gb|AF248662.1|AF248662 Gryllus campestris haplotype 2 cytoc...	50	2e-05
gb|AF248661.1|AF248661 Gryllus campestris haplotype 1 cytoc...	50	2e-05
gb|AF096462.1|AF096462 Rhipidura albicollis cytochrome b ge...	50	2e-05
gb|AF283644.1|AF283644 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283643.1|AF283643 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283642.1|AF283642 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283641.1|AF283641 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283640.1|AF283640 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283639.1|AF283639 Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283637.1|AF283637 Elaphe obsoleta LSUMZ 45359 cytochro...	50	2e-05
gb|AF283636.1|AF283636 Elaphe obsoleta LSUMZ 44662 cytochro...	50	2e-05
gb|AF283635.1|AF283635 Elaphe obsoleta LSUMZ 40443 cytochro...	50	2e-05
gb|AF283634.1|AF283634 Elaphe obsoleta LSUMZ 44335 cytochro...	50	2e-05
gb|AF283633.1|AF283633 Elaphe obsoleta LSUMZ 42624 cytochro...	50	2e-05
gb|AF283632.1|AF283632 Elaphe obsoleta LSUMZ H1911 cytochro...	50	2e-05
gb|AF283631.1|AF283631 Elaphe obsoleta LSUMZ 41197 cytochro...	50	2e-05
gb|AF283630.1|AF283630 Elaphe obsoleta LSUMZ 41189 cytochro...	50	2e-05
gb|AF283629.1|AF283629 Elaphe obsoleta LSUMZ 41188 cytochro...	50	2e-05
gb|AF283628.1|AF283628 Elaphe obsoleta LSUMZ 41187 cytochro...	50	2e-05
gb|AF283627.1|AF283627 Elaphe obsoleta LSUMZ 41186 cytochro...	50	2e-05
gb|AF283626.1|AF283626 Elaphe obsoleta LSUMZ 40943 cytochro...	50	2e-05
gb|AF283625.1|AF283625 Elaphe obsoleta LSUMZ 37499 cytochro...	50	2e-05
gb|AF283624.1|AF283624 Elaphe obsoleta LSUMZ 44480 cytochro...	50	2e-05
gb|AF283623.1|AF283623 Elaphe obsoleta LSUMZ 44451 cytochro...	50	2e-05
gb|AF283622.1|AF283622 Elaphe obsoleta LSUMZ 40444 cytochro...	50	2e-05
gb|AF283621.1|AF283621 Elaphe obsoleta LSUMZ 39925 cytochro...	50	2e-05
gb|AF283620.1|AF283620 Elaphe obsoleta LSUMZ 39163 cytochro...	50	2e-05
gb|AF283619.1|AF283619 Elaphe obsoleta LSUMZ39162 cytochrom...	50	2e-05
gb|AF283618.1|AF283618 Elaphe obsoleta LSUMZ H15896 cytochr...	50	2e-05
gb|AF283617.1|AF283617 Elaphe obsoleta LSUMZ H15892 cytochr...	50	2e-05
gb|AF283616.1|AF283616 Elaphe obsoleta LSUMZ 15891 cytochro...	50	2e-05
gb|AF283615.1|AF283615 Elaphe obsoleta LSUMZ H15890 cytochr...	50	2e-05
gb|AF283614.1|AF283614 Elaphe obsoleta LSUMZ H15887 cytochr...	50	2e-05
gb|AF283613.1|AF283613 Elaphe obsoleta LSUMZ H15888 cytochr...	50	2e-05

gb|AF283612.1|AF283612	Elaphe obsoleta LSUMZ H15884 cytochr...	50	2e-05
gb|AF283611.1|AF283611	Elaphe obsoleta LSUMZ H15031 cytochr...	50	2e-05
gb|AF283610.1|AF283610	Elaphe obsoleta LSUMZ H15030 cytochr...	50	2e-05
gb|AF283609.1|AF283609	Elaphe obsoleta CAS 169468 cytochrom...	50	2e-05
gb|AF283608.1|AF283608	Elaphe obsoleta LSUMZ H14782 cytochr...	50	2e-05
gb|AF283607.1|AF283607	Elaphe obsoleta LSUMZ H14781 cytochr...	50	2e-05
gb|AF283606.1|AF283606	Elaphe obsoleta LSUMZ H14724 cytochr...	50	2e-05
gb|AF283605.1|AF283605	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283604.1|AF283604	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283603.1|AF283603	Elaphe obsoleta cytochrome b gene, c...	50	2e-05
gb|AF283602.1|AF283602	Elaphe obsoleta LSUMZ H3388 cytochro...	50	2e-05
gb|AF283601.1|AF283601	Elaphe obsoleta LSUMZ H3385 cytochro...	50	2e-05
gb|AF283600.1|AF283600	Elaphe obsoleta LSUMZ H3384 cytochro...	50	2e-05
gb|AF283599.1|AF283599	Elaphe bairdi LSUMZ H3382 cytochrome...	50	2e-05
gb|AF283598.1|AF283598	Elaphe bairdi LSUMZ H3381 cytochrome...	50	2e-05
gb|AF283597.1|AF283597	Elaphe obsoleta LSUMZ H3379 cytochro...	50	2e-05
gb|AF283596.1|AF283596	Elaphe obsoleta LSUMZ 39616 cytochro...	50	2e-05
gb|AF283595.1|AF283595	Elaphe obsoleta LSUMZ H3376 cytochro...	50	2e-05
gb|AF283594.1|AF283594	Elaphe obsoleta LSUMZ H3345 cytochro...	50	2e-05
gb|AF283593.1|AF283593	Elaphe obsoleta LSUMZ H3309 cytochro...	50	2e-05
gb|AF283592.1|AF283592	Elaphe obsoleta LSUMZ H3306 cytochro...	50	2e-05
gb|AF283591.1|AF283591	Elaphe obsoleta LSUMZ H3276 cytochro...	50	2e-05
gb|AF283590.1|AF283590	Elaphe obsoleta LSUMZ H3246 cytochro...	50	2e-05
gb|AF283589.1|AF283589	Elaphe obsoleta LSUMZ H3212 cytochro...	50	2e-05
gb|AF283588.1|AF283588	Elaphe obsoleta LSUMZ H3209 cytochro...	50	2e-05
gb|AF283587.1|AF283587	Elaphe obsoleta LSUMZ H3206 cytochro...	50	2e-05
gb|AF283586.1|AF283586	Elaphe obsoleta LSUMZ H3191 cytochro...	50	2e-05
gb|AF283585.1|AF283585	Elaphe obsoleta LSUMZ H3190 cytochro...	50	2e-05
gb|AF283584.1|AF283584	Elaphe obsoleta LSUMZ H3189 cytochro...	50	2e-05
gb|AF283583.1|AF283583	Elaphe obsoleta LSUMZ H3188 cytochro...	50	2e-05
gb|AF283582.1|AF283582	Elaphe obsoleta LSUMZ H3186 cytochro...	50	2e-05
gb|AF283581.1|AF283581	Elaphe obsoleta LSUMZ H3169 cytochro...	50	2e-05
gb|AF283580.1|AF283580	Elaphe obsoleta CAS 203083 cytochrom...	50	2e-05
gb|AF283579.1|AF283579	Elaphe obsoleta CAS 203079 cytochrom...	50	2e-05
gb|AF283578.1|AF283578	Elaphe obsoleta LSUMZ H2286 cytochro...	50	2e-05
gb|AF283577.1|AF283577	Elaphe obsoleta CAS 208631 cytochrom...	50	2e-05
gb|AF283576.1|AF283576	Elaphe obsoleta LSUMZ H2229 cytochro...	50	2e-05
gb|AF187030.1|AF187030	Rhinophylla pumilio isolate TK46001 ...	50	2e-05
gb|AF310052.1|AF310052	Poospiza hispaneolensis cytochrome b...	50	2e-05
gb|AF310046.1|AF310046	Volatinia jacarina cytochrome b gene...	50	2e-05
gb|AF171919.1|AF171919	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb|AF171897.1|AF171897	Trimeresurus mucrosquamatus cytb gen...	50	2e-05
gb|AF290174.1|AF290174	Agelaius cyanopus cytochrome b (cytb...	50	2e-05
gb|AF290173.1|AF290173	Agelaius phoeniceus cytochrome b (cy...	50	2e-05
gb|AF290171.1|AF290171	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb|AF290170.1|AF290170	Amblycercus holosericeus cytochrome ...	50	2e-05
gb|AF290150.1|AF290150	Volatinia jacarina cytochrome b (cyt...	50	2e-05
gb|AF176252.1|AF176252	Reithrodontomys zacatecae cytochrome...	50	2e-05
gb|AF176251.1|AF176251	Reithrodontomys zacatecae cytochrome...	50	2e-05
gb|AF163907.1|AF163907	Microtus xanthognathus cytochrome b ...	50	2e-05
gb|AF163904.1|AF163904	Microtus pinetorum cytochrome b gene...	50	2e-05
gb|AF163901.1|AF163901	Microtus ochrogaster cytochrome b ge...	50	2e-05
gb|AF163899.1|AF163899	Microtus miurus cytochrome b gene, c...	50	2e-05
gb|AF163891.1|AF163891	Microtus californicus cytochrome B (...	50	2e-05
gb|AF163890.1|AF163890	Microtus abbreviatus cytochrome B (c...	50	2e-05
gb|AF288524.1|AF288524	Dipsochelys dussumieri isolate Germa...	50	2e-05
gb|AF288523.1|AF288523	Dipsochelys dussumieri isolate white...	50	2e-05
gb|AF288522.1|AF288522	Dipsochelys dussumieri isolate Aldy ...	50	2e-05
gb|AF123530.1|AF123530	Psilopogon pyrolophus cytochrome b (...	50	2e-05
gb|AF123512.1|AF123512	Eubucco bourcierii tucinkae cytochro...	50	2e-05
gb|AF206548.1|AF206548	Adolfus vauereselli cytochrome b gen...	50	2e-05
gb|AF197867.1|AF197867	Gymnorhina tibicen cytochrome b gene...	50	2e-05
gb|U63397.2|SEU63397	Sitta europaea cytochrome b gene, part...	50	2e-05
ref|NC_001945.1|	Dinodon semicarinatus mitochondrion, compl...	50	2e-05
ref|NC_001821.1|	Dasypus novemcinctus mitochondrion, comple...	50	2e-05
gb|AF141217.1|AF141217	Dasymys incomtus country Tanzania cy...	50	2e-05
gb|AF201615.1|AF201615	Pantodon buchholzi cyotchrome b gene...	50	2e-05
gb|AF077920.1|AF077920	Bombus nevadensis cytochrome b gene,...	50	2e-05
gb|AF190612.1|AF190612	Oreamnos americanus cytochrome b (cy...	50	2e-05
gb|J01394.1|BOVMT	Bos taurus mitochondrion, complete genome	50	2e-05
gb|AF191810.1|AF191810	Cochlearius cochlearius cytochrome b...	50	2e-05

gb|U89181.1|CAU89181	Chlorostilbon aureoventris cytochrome ...	50	2e-05
gb|U89171.1|AFU89171	Asio flammeus cytochrome b (cytb) gene...	50	2e-05
gb|AF217833.1|AF217833	Homoroselaps lacteus cytochrome b ge...	50	2e-05
gb|AF217822.1|AF217822	Hydrophis semperi cytochrome b gene,...	50	2e-05
gb|AF217813.1|AF217813	Acanthophis antarcticus cytochrome b...	50	2e-05
gb|AF220408.1|AF220408	Calliophis kelloggi cytochrome b (cy...	50	2e-05
gb|AF126430.1|AF126430	Ellobius fuscocapillus cytochrome b ...	50	2e-05
gb|AF090337.1|AF090337	Aythya americana mitochondrion, comp...	50	2e-05
gb|AF059111.1|AF059111	Sarkidiornis melanotos cytochrome b ...	50	2e-05
gb|AF059053.1|AF059053	Aix sponsa cytochrome b gene, partia...	50	2e-05
gb|AF099308.1|AF099308	Icterus wagleri wagleri cytochrome b...	50	2e-05
gb|AF099295.1|AF099295	Icterus gularis yucatanensis cytochr...	50	2e-05
gb|AF099294.1|AF099294	Icterus gularis tamaulipensis cytoch...	50	2e-05
gb|AF099293.1|AF099293	Icterus gularis gularis cytochrome b...	50	2e-05
gb|AF160610.1|AF160610	Cricetomys emini Cemi636 cytochrome ...	50	2e-05
gb|AF036280.1|AF036280	Tragelaphus strepsiceros cytochrome ...	50	2e-05
gb|AF036277.1|AF036277	Tragelaphus scriptus cytochrome b (c...	50	2e-05
gb|AF036274.1|	Tetracerus quadricornis cytochrome b (cytb) ...	50	2e-05
gb|AF194218.1|AF194218	Phrynosoma platyrhinos cytochrome b ...	50	2e-05
gb|AF194216.1|AF194216	Urosaurus ornatus cytochrome b gene,...	50	2e-05
ref|NC_002009.1|	Artibeus jamaicensis mitochondrion, comple...	50	2e-05
ref|NC_001941.1|	Ovis aries mitochondrion, complete genome	50	2e-05
ref|NC_000877.1|	Aythya americana mitochondrion, complete g...	50	2e-05
ref|NC_000846.1|	Rhea americana mitochondrion, complete genome	50	2e-05
gb|U27551.1|GCU27551	Grus canadensis tabida cytochrome b (c...	50	2e-05
gb|AF089058.1|AF089058	Quiscalus quiscula cytochrome b (cyt...	50	2e-05
gb|AF089055.1|AF089055	Quiscalus major cytochrome b (cytb) ...	50	2e-05
gb|AF089054.1|AF089054	Quiscalus lugubris cytochrome b (cyt...	50	2e-05
gb|AF089046.1|AF089046	Oreopsar bolivianus cytochrome b (cy...	50	2e-05
gb|AF089042.1|AF089042	Molothrus badius cytochrome b (cytb)...	50	2e-05
gb|AF089039.1|AF089039	Macroagelaius imthurni cytochrome b ...	50	2e-05
gb|AF089037.1|AF089037	Lampropsar tanagrinus cytochrome b (...	50	2e-05
gb|AF089026.1|AF089026	Gymnomystax mexicanus cytochrome b (...	50	2e-05
gb|AF089025.1|AF089025	Gnorimopsar chopi cytochrome b (cytb...	50	2e-05
gb|AF089024.1|AF089024	Euphagus cyanocephalus cytochrome b ...	50	2e-05
gb|AF089023.1|AF089023	Euphagus carolinus cytochrome b (cyt...	50	2e-05
gb|AF089021.1|AF089021	Dives warszewiczi cytochrome b (cyt...	50	2e-05
gb|AF089020.1|AF089020	Curaeus curaeus cytochrome b (cytb) ...	50	2e-05
gb|AF089016.1|AF089016	Amblycercus holosericeus cytochrome ...	50	2e-05
gb|AF089013.1|AF089013	Agelaius xanthophthalmus cytochrome ...	50	2e-05
gb|AF089012.1|AF089012	Agelaius xanthomus cytochrome b (cyt...	50	2e-05
gb|AF089008.1|AF089008	Agelaius phoeniceus sub-species phoe...	50	2e-05
gb|AF089006.1|AF089006	Agelaius humeralis cytochrome b (cyt...	50	2e-05
gb|AF089005.1|AF089005	Agelaius cyanopus cytochrome b (cytb...	50	2e-05
gb|AF108696.1|AF108696	Scolomys juruaense cytochrome B (cyt...	50	2e-05
gb|AF108685.1|AF108685	Wiedomys pyrrhorhinos cytochrome B (...	50	2e-05
gb|AF108677.1|AF108677	Thomasomys oreas cytochrome B (cytB)...	50	2e-05
gb|AF145531.1|AF145531	Melanoplus foedus cytochrome b gene,...	50	2e-05
gb|AF145511.1|AF145511	Melanoplus angustipennis cytochrome ...	50	2e-05
gb|U89627.1|BMU89627	Bolitoglossa marmorea cytochrome b (cy...	50	2e-05
gb|U89623.1|BPU89623	Batrachoseps pacificus cytochrome b (c...	50	2e-05
gb|AF181470.1|AF181470	Okapia johnstoni cytochrome b gene, ...	50	2e-05
gb|AF084075.1|AF084075	Lagenorhynchus acutus cytochrome b g...	50	2e-05
gb|U90303.1|OMU90303	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb|U90302.1|OMU90302	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb|U90301.1|OMU90301	Ovibos moschatus cytochrome b (cytb)| g...	50	2e-05
gb|U90300.1|OMU90300	Ovibos moschatus cytochrome b (cytb) g...	50	2e-05
gb|AF038883.1|AF038883	Deinagkistrodon acutus cytochrome b ...	50	2e-05
gb|AF039268.1|AF039268	Agkistrodon contortrix cytochrome b ...	50	2e-05
gb|AF039267.1|AF039267	Boa constrictor cytochrome b (cytb) ...	50	2e-05
gb|S49215.1|S49215	apocytochrome b (sheep, domestic, Merino...	50	2e-05
gb|AF158698.1|AF158698	Geomys pinetis cytochrome b gene, co...	50	2e-05
gb|AF158692.1|AF158692	Geomys bursarius jugossicularis cyto...	50	2e-05
gb|AF068193.1|AF068193	Ithaginis cruentus cytochrome b (cyt...	50	2e-05
gb|AF091629.1|AF091629	Antilocapra americana cytochrome b (...	50	2e-05
gb|AF022063.1|	Tragelaphus strepsiceros cytochrome b (cytb)...	50	2e-05
gb|AF022062.1|	Tragelaphus derbianus cytochrome b (cytb) ge...	50	2e-05
gb|AF022060.1|	Hippotragus equinus cytochrome b (cytb) gene...	50	2e-05
gb|AF022057.1|	Tragelaphus oryx cytochrome b (cytb) gene, m...	50	2e-05
gb|AF113500.1|AF113500	Lagenorhynchus acutus isolate LAC034...	50	2e-05
gb|AF113499.1|AF113499	Lagenorhynchus acutus isolate LAC0?) .	50	2e-05

gb|U69645.1|LBU69645	Loxocemus bicolor cytochrome b (cytb) ...	50	2e-05
gb|U69810.1|ENU69810	Eunectes notaeus cytochrome b (cytb) g...	50	2e-05
gb|U69808.1|EMU69808	Eunectes murinus cytochrome b (cytb) g...	50	2e-05
gb|U69799.1|ESU69799	Epicrates striatus fosteri cytochrome ...	50	2e-05
gb|U69796.1|ESU69796	Epicrates striatus strigilatus cytochr...	50	2e-05
gb|U69795.1|ESU69795	Epicrates striatus strigilatus cytochr...	50	2e-05
gb|U69794.1|ESU69794	Epicrates striatus mccraniei cytochrom...	50	2e-05
gb|U69793.1|ESU69793	Epicrates striatus mccraniei cytochrom...	50	2e-05
gb|U69792.1|EMU69792	Epicrates monensis cytochrome b (cytb)...	50	2e-05
gb|U69790.1|EMU69790	Epicrates monensis cytochrome b (cytb)...	50	2e-05
gb|U69786.1|EFU69786	Epicrates fordi cytochrome b (cytb) ge...	50	2e-05
gb|U69784.1|EFU69784	Epicrates fordi cytochrome b (cytb) ge...	50	2e-05
gb|U69779.1|ECU69779	Epicrates cenchria cytochrome b (cytb)...	50	2e-05
gb|U69777.1|ECU69777	Epicrates cenchria cytochrome b (cytb)...	50	2e-05
gb|U69776.1|EAU69776	Epicrates angulifer cytochrome b (cytb...	50	2e-05
gb|U69774.1|EAU69774	Epicrates angulifer cytochrome b (cytb...	50	2e-05
gb|U69772.1|CEU69772	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb|U69771.1|CEU69771	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb|U69770.1|CEU69770	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb|U69769.1|CEU69769	Corallus enydris cytochrome b (cytb) g...	50	2e-05
gb|U69752.1|CAU69752	Candoia aspera cytochrome b (cytb) gen...	50	2e-05
gb|U69746.1|BCU69746	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
gb|U69740.1|BCU69740	Boa constrictor cytochrome b (cytb) ge...	50	2e-05
gb|AF139057.1|AF139057	Isoodon macrourus cytochrome b gene,...	50	2e-05
gb|AF090339.1|AF090339	Rhea americana mitochondrion, comple...	50	2e-05
gb|AF006275.1|AF006275	Cnemidophorus tigris strain Isla Ang...	50	2e-05
gb|AF006267.1|AF006267	Cnemidophorus tigris strain Isla Smi...	50	2e-05
gb|AF034969.1|AF034969	Connochaetes taurinus cytochrome b g...	50	2e-05
gb|AF028822.1|AF028822	Alcelaphus buselaphus cytochrome b g...	50	2e-05
gb|AF028821.1|AF028821	Damaliscus lunatus cytochrome b gene...	50	2e-05
gb|AF061340.1|AF061340	Artibeus jamaicensis mitochondrial D...	50	2e-05
gb|AF076093.1|AF076093	Thalassarche impavida cytochrome b (...	50	2e-05
gb|AF076091.1|AF076091	Thalassarche carteri cytochrome b (c...	50	2e-05
gb|AF076072.1|AF076072	Pelagodroma marina cytochrome b (cyt...	50	2e-05
gb|AF076063.1|AF076063	Oceanodroma furcata cytochrome b (cy...	50	2e-05
gb|AF076059.1|AF076059	Hydrobates pelagicus cytochrome b (c...	50	2e-05
gb|AF076056.1|AF076056	Garrodia nereis cytochrome b (cytb) ...	50	2e-05
gb|AF076053.1|AF076053	Fregetta tropica cytochrome b (cytb)...	50	2e-05
gb|AF076050.1|AF076050	Diomedea gibsoni cytochrome b (cytb)...	50	2e-05
gb|AF076049.1|AF076049	Diomedea epomophora cytochrome b (cy...	50	2e-05
gb|AF076048.1|AF076048	Diomedea chionoptera cytochrome b (c...	50	2e-05
gb|AF076047.1|AF076047	Diomedea antipodensis cytochrome b (...	50	2e-05
gb|U83314.1|MSU83314	Micrastur semitorquatus cytochrome b (...	50	2e-05
gb|U83318.1|MEU83318	Microhierax erythrogenys cytochrome b ...	50	2e-05
gb|U37303.1|SAU37303	Synthliboramphus antiquus cytochrome b...	50	2e-05
gb|U37302.1|PAU37302	Ptychoramphus aleuticus cytochrome b g...	50	2e-05
gb|U37296.1|CPU37296	Cyclorrhynchus psittacula cytochrome b...	50	2e-05
gb|U37289.1|BBU37289	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb|U37286.1|APU37286	Aethia pygmaea cytochrome b gene, mito...	50	2e-05
gb|U37104.1|APU37104	Aethia pusilla cytochrome b gene, mito...	50	2e-05
gb|U37087.1|ACU37087	Aethia cristatella cytochrome b gene, ...	50	2e-05
gb|U87525.1|HGU87525	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb|U87524.1|HGU87524	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb|U87523.1|HGU87523	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb|U87522.1|HGU87522	Heterocephalus glaber cytochrome-b gen...	50	2e-05
gb|U17864.1|STU17864	Saiga tatarica cytochrome b gene, mito...	50	2e-05
gb|U17863.1|OAU17863	Oreamnos americanus cytochrome b gene....	50	2e-05
gb|U17862.1|OMU17862	Ovibos moschatus moschatus cytochrome ...	50	2e-05
gb|U17860.1|ODU17860	Ovis dalli cytochrome b gene, mitochon...	50	2e-05
gb|U17859.1|OCU17859	Ovis canadensis cytochrome b gene, mit...	50	2e-05
gb|U65274.1|TBU65274	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb|U65267.1|TBU65267	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb|U65260.1|TBU65260	Thomomys bottae cytochrome b (cytb) ge...	50	2e-05
gb|U65301.1|PAU65301	Perognathus amplus cytochrome b (cytb)...	50	2e-05
gb|AF034739.1|AF034739	Capra aegagrus cytochrome b (cytb) g...	50	2e-05
gb|AF034738.1|	Capra caucasica cytochrome b (cytb) gene, mi...	50	2e-05
gb|AF034737.1|	Capra cylindricornis cytochrome b (cytb) gen...	50	2e-05
gb|AF034736.1|AF034736	Capra falconeri cytochrome b (cytb) ...	50	2e-05
gb|AF034735.1|	Capra ibex cytochrome b (cytb) gene, mitocho...	50	2e-05
gb|AF034730.1|AF034730	Ovis aries cytochrome b (cytb) gene...	50	2e-05
gb|AF034729.1|AF034729	Ovis vignei cytochrome b (cytb) gene	50	2e-05

gb|AF034728.1| Ovis dalli dalli cytochrome b (cytb) gene, m...	50	2e-05
gb|AF034727.1| Ovis ammon darwini cytochrome b (cytb) gene....	50	2e-05
gb|AF034724.1|AF034724 Pantholops hodgsoni cytochrome b (cy...	50	2e-05
gb|AF057132.1|AF057132 Taxidea taxus cytochrome b (cytb) ge...	50	2e-05
gb|U94805.1|TMU94805 Trogon melanurus cytochrome b gene, mi...	50	2e-05
gb|U94804.1|TCU94804 Trogon comptus cytochrome b gene, mito...	50	2e-05
gb|U94803.1|TVU94803 Trogon viridis cytochrome b gene, mito...	50	2e-05
gb|AF006251.1|AF006251 Sericossypha albocristata cytochrome...	50	2e-05
gb|AF006249.1|AF006249 Pyrrhocoma ruficeps cytochrome b (cy...	50	2e-05
gb|AF006238.1|AF006238 Lamprospiza melanoleuca cytochrome b...	50	2e-05
gb|AF006234.1|AF006234 Hemispingus atropileus cytochrome b ...	50	2e-05
gb|AF006226.1|AF006226 Cypsnagra hirundinacea cytochrome b ...	50	2e-05
gb|AF006215.1|AF006215 Chlorophanes spiza cytochrome b (cyt...	50	2e-05
gb|AF006214.1|AF006214 Chlorochrysa calliparaea cytochrome ...	50	2e-05
gb|AF006213.1|AF006213 Calochaetes coccineus cytochrome b (...	50	2e-05
gb|AF006212.1|AF006212 Buthraupis montana cytochrome b (cyt...	50	2e-05
emb|AJ293419.1|RRU293419 Rupicapra rupicapra rupicapra mito...	50	2e-05
emb|AJ293416.1|RPY293416 Rupicapra pyrenaica pyrenaica mito...	50	2e-05
emb|AJ293415.1|RPY293415 Rupicapra pyrenaica parva mitochon...	50	2e-05
emb|AJ293414.1|RPY293414 Rupicapra pyrenaica ornata mitocho...	50	2e-05
emb|AJ293412.1|RRU293412 Rupicapra rupicapra rupicapra mito...	50	2e-05
emb|AJ293418.1|CFA293418 Capra falconeri mitochondrial part...	50	2e-05
gb|U07578.1|DCU07578 Dasycercus cristicauda mitochondrion c...	50	2e-05
emb|AJ004180.1|HPAJ4180 Hydrobates pelagicus mitochondrial ...	50	2e-05
emb|Y15695.1|SMY15695 Schilbe mystus mitochondrial cytb gen...	50	2e-05
emb|Y15697.1|EDY15697 Eutropius depressirostris mitochondri...	50	2e-05
emb|Y15696.1|EDY15696 Eutropius depressirostris mitochondri...	50	2e-05
gb|AF015035.1|AF015035 Steatocranus casuarinus 20 cytochrom...	50	2e-05
gb|AF015761.1|AF015761 Palmeria dolei cytochrome b (Cytb) g...	50	2e-05
gb|AF015758.1|AF015758 Oreomystis mana cytochrome b (Cytb) ...	50	2e-05
gb|AF015756.1|AF015756 Vestiaria coccinea cytochrome b (Cyt...	50	2e-05
gb|AF015754.1|AF015754 Himatione sanguinea cytochrome b (Cy...	50	2e-05
gb|U76052.1|DNU76052 Dromaius novaehollandiae cytochrome b ...	50	2e-05
emb|AJ236834.1|CGL236834 Clethrionomys glareolus mitochondr...	50	2e-05
gb|U83158.1|POU83158 Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb|U83157.1|POU83157 Pelecanus onocrotalus cytochrome B gen...	50	2e-05
gb|U83156.1|AAU83156 Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb|U83155.1|AAU83155 Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb|U83154.1|AAU83154 Anhinga anhinga cytochrome B gene, mit...	50	2e-05
gb|U81356.1|CLU81356 Chelodina longicollis cytochrome b gen...	50	2e-05
emb|AJ277676.1|ESC277676 Elaphe scalaris mitochondrial part...	50	2e-05
emb|AJ277675.1|ESC277675 Elaphe scalaris mitochondrial part...	50	2e-05
emb|AJ277672.1|ELO277672 Elaphe longissima mitochondrial pa...	50	2e-05
emb|AJ277671.1|ELO277671 Elaphe longissima mitochondrial pa...	50	2e-05
emb|Y11832.1|MTDNCOMGN Dasypus novemcinctus complete mitoch...	50	2e-05
emb|AJ388467.1|NBA388467 Nemacheilus barbatulus mitochondria...	50	2e-05
emb|AJ388468.1|IME388468 Ictalurus melas mitchondrial cyt b...	50	2e-05
emb|AJ388459.1|LDE388459 Leucaspius delineatus mitchondrial...	50	2e-05
gb|U46167.1|SCU46167 Sciurus carolinensis cytochrome b gene...	50	2e-05
emb|AJ245673.1|SIN245673 Schilbe intermedius partial mitoch...	50	2e-05
emb|AJ245638.1|SIN245638 Schilbe intermedius partial mitoch...	50	2e-05
emb|AJ245678.1|EDE245678 Eutropius depressirostris partial ...	50	2e-05
emb|AJ245677.1|EDE245677 Eutropius depressirostris partial ...	50	2e-05
emb|AJ245676.1|EDE245676 Eutropius depressirostris partial ...	50	2e-05
emb|AJ245675.1|EDE245675 Eutropius depressirostris partial ...	50	2e-05
emb|AJ245674.1|EDE245674 Eutropius depressirostris partial ...	50	2e-05
emb|Y16884.3|MTRACOMPL Rhea americana complete mitochondria....	50	2e-05
gb|U60768.1|PCU60768 Parus cinctus cytochrome b gene, mitoc...	50	2e-05
gb|U48955.1|TMU48955 Thalassarche melanophris melanophris c...	50	2e-05
gb|U48954.1|TCU48954 Thalassarche chrysostoma cytochrome b ...	50	2e-05
gb|U48944.1|TCU48944 Thalassarche chlororhynchos chlororhyn...	50	2e-05
gb|U48943.1|PPU48943 Phoebetria palpebrata cytochrome b (cy...	50	2e-05
gb|U48942.1|PFU48942 Phoebetria fusca cytochrome b (cytb) g...	50	2e-05
gb|U48941.1|MGU48941 Macronectes giganteus cytochrome b (cy...	50	2e-05
gb|U48947.1|DEU48947 Diomedea exulans dabbenena cytochrome ...	50	2e-05
gb|U48946.1|DEU48946 Diomedea epomophora sanfordi cytochrom...	50	2e-05
gb|U48948.1|DAU48948 Diomedea amsterdamensis cytochrome b (...	50	2e-05
gb|U15725.1|PRU15725 Piranga rubra cytochrome b gene, mitoc...	50	2e-05
gb|U66508.1|APU66508 Artibeus planirostris cytochrome b (cy...	50	2e-05
gb|U66507.1|AOU66507 Artibeus obscurus cytochrome b (cytb) ...	50	2e-05
gb|U66506.1|AOU66506 Artibeus obscurus cytochrome b (cytb) ...	50	2e-05

gb|U66505.1|ALU66505	Artibeus lituratus cytochrome b (cytb)...	50	2e-05
gb|U66504.1|AJU66504	Artibeus jamaicensis cytochrome b (cyt...	50	2e-05
gb|U66503.1|AJU66503	Artibeus jamaicensis cytochrome b (cyt...	50	2e-05
gb|U66502.1|AIU66502	Artibeus intermedius cytochrome b (cyt...	50	2e-05
gb|U66501.1|AIU66501	Artibeus inopinatus cytochrome b (cytb...	50	2e-05
gb|U66500.1|AHU66500	Artibeus hirsutus cytochrome b (cytb) ...	50	2e-05
gb|U66499.1|AFU66499	Artibeus fraterculus cytochrome b (cyt...	50	2e-05
gb|U66498.1|AFU66498	Artibeus fimbriatus cytochrome b (cytb...	50	2e-05
gb|U63061.1|BBU63061	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb|U63060.1|BBU63060	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb|U63059.1|BBU63059	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb|U63058.1|BBU63058	Brachyramphus brevirostris cytochrome ...	50	2e-05
gb|U58386.1|SJU58386	Scolomys juruaense cytochrome b (cyt-b...	50	2e-05
gb|L11905.1|CGYMTCYTBD	Cratogeomys gymnurus mitochondrial c...	50	2e-05
gb|U34672.1|MNU34672	Metachirus nudicaudatus cytochrome b 1...	50	2e-05
gb|U34671.1|MNU34671	Metachirus nudicaudatus cytochrome b 1...	50	2e-05
emb|Y14951.1|MTY14951	Capreolus capreolus mitochondrial cyt...	50	2e-05
emb|Y14371.1|MTCCCYTB	Capreolus capreolus mitochondrial cyt...	50	2e-05
gb|L11909.1|CGYMTCYTBH	Cratogeomys tylorhinus mitochondrial...	50	2e-05
gb|L11901.1|PPGMTCYTBB	Geomys bursarius juggosicularis mito...	50	2e-05
gb|L11904.1|CGYMTCYTBC	Cratogeomys goldmani goldmani mitoch...	50	2e-05
emb|X94928.1|SPCYTB	S.putorius mitochondrial DNA for cytoch...	50	2e-05
gb|U46770.1|ARU46770	Anthus richardi cytochrome b gene, mit...	50	2e-05
gb|U46769.1|ABU46769	Anthus berthelotii cytochrome b gene, ...	50	2e-05
gb|U46183.1|SSU46183	Sciurus stramineus cytochrome b gene, ...	50	2e-05
emb|Y10728.1|PSMY10728	P.schwarzi mitochondrial cytb gene, ...	50	2e-05
emb|X95768.1|NLMCB	N.leucopterus mitochondrial cytochrome b...	50	2e-05
emb|X95767.1|NGRIMCB	N.griseus mitochondrial cytochrome b gene	50	2e-05
emb|X86763.1|MTVGCYT26	V.gryphus mitochondrial cytb gene	50	2e-05
emb|X86754.1|MTLCCYT17	L.crumeniferus mitochondrial cytb gene	50	2e-05
emb|X86743.1|MTCACYT6	C.aura mitochondrial cytb gene	50	2e-05
dbj|AB035242.1|AB035242	Pantodon buchholzi mitochondrial cy...	50	2e-05
emb|X60946.1|MITDCB33	T. dorbignyi mitochondrial gene for c...	50	2e-05
emb|AJ000029.1|MIRTCYB29	Rangifer tarandus mitochondrial cy...	50	2e-05
emb|X82302.1|MIPFCYTBG	P.fasciata mitochondrial cytochrome ...	50	2e-05
emb|X56291.1|MIOHCYTB	O.hemionus mitochondrion cytb gene fo...	50	2e-05
emb|X56284.1|MIOACYTB	O.aries mitochondrion cytb gene for c...	50	2e-05
emb|AJ000022.1|MIMSCYB22	Dama dama mitochondrial cytb gene	50	2e-05
emb|X72005.1|MILWCYTB	L.weddelli mitochondrial gene for cyt...	50	2e-05
emb|Y08814.1|MIHLCYTBG	H.liberiensis mitochondrial cytochro...	50	2e-05
emb|X60942.1|MIGTCB33	Gymnorhina tibicen mitochondrial gene...	50	2e-05
emb|X56290.1|MIDDCYTB	D.dama mitochondrion cytb gene for cy...	50	2e-05
emb|AJ000021.1|MICECYB21	Cervus elaphus mitochondrial cytb ...	50	2e-05
emb|AJ000024.1|MICCCYB24	Capreolus capreolus mitochondrial ...	50	2e-05
emb|V00654.1|MIBTXX	Bos taurus complete mitochondrial genome	50	2e-05
emb|X56286.1|MIAACYTBA	A.americana mitochondrion cytb gene ...	50	2e-05
gb|L19718.1|AIUMTCYTB	Artibeus lituratus mitochondrial cyto...	50	2e-05
gb|U27543.1|BRU27543	Balearica regulorum cytochrome b (cytb...	50	2e-05
dbj|AB030025.1|AB030025	Sciurus stramineus mitochondrial cy...	50	2e-05
gb|U18258.1|SCU18258	Spharagemon campestris cytochrome b ge...	50	2e-05
gb|U18257.1|SCU18257	Spharagemon collare cytochrome b gene,...	50	2e-05
gb|U18253.1|TPU18253	Trimerotropis pistrinaria cytochrome b...	50	2e-05
gb|U18250.1|CPU18250	Camnula pellucida cytochrome b gene, m...	50	2e-05
gb|U17904.1|CCU17904	Circotettix carlinianus mitochondrion ...	50	2e-05
dbj|D84202.1|GOTMTCBB	Capra falconeri mitochondrial DNA for...	50	2e-05
dbj|D82889.1|D82889	Bos javanicus mitochondrial DNA for cyt...	50	2e-05
dbj|D32195.1|CCRMTCB25	Capricornis sumatrensis mitochodrial...	50	2e-05
dbj|D32191.1|CCRMTCB21	Capricornis crispus mitochondrial ge...	50	2e-05
dbj|AB021098.1|AB021098	Cervus elaphus kansuensis mitochond...	50	2e-05
dbj|AB021097.1|AB021097	Cervus elaphus xanthopygus mitochon...	50	2e-05
dbj|AB021095.1|AB021095	Cervus nippon yesoensis mitochondri...	50	2e-05
dbj|AB021094.1|AB021094	Cervus nippon centralis mitochondri...	50	2e-05
dbj|AB021092.1|AB021092	Cervus nippon mageshimae mitochondr...	50	2e-05
dbj|AB021091.1|AB021091	Cervus nippon keramae mitochondrial...	50	2e-05
dbj|AB001612.1|AB001612	Cervus elaphus mitochondrial DNA fo...	50	2e-05
dbj|D84205.1|SHPMTCBE	Sheep mitochondrial DNA for cytochrom...	50	2e-05
dbj|D84203.1|SHPMTCBC	Ovis musimon mitochondrial DNA for cy...	50	2e-05
dbj|D34636.1|BOVMTCBB	Bos javanicus mitochondrial gene for ...	50	2e-05
dbj|D34635.1|BOVMTCBA	Bovine mitochondrial gene for cytochr...	50	2e-05
dbj|D32198.1|ORMMTCB28	Oreamnos americanus mitochondrial ge...	50	2e-05
dbj|D32195.1|NAGMTCB26	Nemorhaedus goral mitochondrial gene...	50	2e-05

		50	2e-05
dbj|D32192.1|CEUMTCB12	Cervus nippon mitochondrial gene for...	50	2e-05
dbj|AB021099.1|AB021099	Cervus elaphus scoticus mitochondri...	50	2e-05
dbj|AB021096.1|AB021096	Cervus elaphus canadensis mitochond...	50	2e-05
dbj|AB021093.1|AB021093	Cervus nippon nippon mitochondrial ...	50	2e-05
dbj|AB021090.1|AB021090	Cervus nippon pulchellus mitochondr...	50	2e-05
dbj|AB008539.1|AB008539	Dinodon semicarinatus mitochondrial...	50	2e-05
dbj|AB006800.1|AB006800	Ovis aries mitochondrial DNA for cy...	50	2e-05
gb|L12763.1|LDHMTCYTB	Lepidochelys kempi (LK-3) mitochondri...	50	2e-05
gb|L08032.1|CPLMTCYTBA	Carcharhinus plumbeus mitochondrial ...	50	2e-05
gb|L28941.1|URRCYB	Uroderma bilobatum cytochrome b gene, 5'...	50	2e-05
gb|L28937.1|CDECYB	Chiroderma doriae cytochrome b gene, 5' end	50	2e-05
emb|AJ010056.1|CPY010056	Capra pyrenaica (individual 12) mi...	50	2e-05
emb|AJ010054.1|CPY010054	Capra pyrenaica (individual 11) mi...	50	2e-05
emb|AJ010053.1|CPY010053	Capra pyrenaica (individual 10) mi...	50	2e-05
emb|AJ010052.1|CPY010052	Capra pyrenaica (individual 9) mit...	50	2e-05
emb|AJ010051.1|CPY010051	Capra pyrenaica (individual 8) mit...	50	2e-05
emb|AJ010050.1|CPY010050	Capra pyrenaica (individual 7) mit...	50	2e-05
emb|AJ010049.1|CPY010049	Capra pyrenaica (individual 6) mit...	50	2e-05
emb|AJ010048.1|CPY010048	Capra pyrenaica (individual 5) mit...	50	2e-05
emb|AJ010047.1|CPY010047	Capra pyrenaica (individual 4) mit...	50	2e-05
emb|X95777.1|CLMCB	C.longirostris mitochondrial cytochrome ...	50	2e-05
emb|AJ009879.1|CIB9879	Capra ibex nubiana mitochondrial cyt...	50	2e-05
emb|AJ010055.1|CIB010055	Capra ibex (individual 1) ibex mit...	50	2e-05
gb|U08946.1|CAU08946	Coragyps atratus mitochondrion cytochr...	50	2e-05
gb|U08945.1|CBU08945	Cathartes burrovianus mitochondrion cy...	50	2e-05
gb|U08944.1|VGU08944	Vultur gryphus mitochondrion cytochrom...	50	2e-05
gb|U08941.1|PAU08941	Platalea alba mitochondrion cytochrome...	50	2e-05
gb|U08940.1|PRU08940	Phoenicopterus ruber mitochondrion cyt...	50	2e-05
emb|X95775.1|ACMCB	A.cristatus mitochondrial cytochrome b gene	50	2e-05
emb|X95774.1|ABMCB	A.bennettii mitochondrial cytochrome b gene	50	2e-05
emb|X95764.1|AAMCB	A.albertisi mitochondrial cytochrome b gene	50	2e-05
gb|AF040383.1|AF040383	Alces alces cytochrome b (cytb) gene...	48	8e-05
gb|AF232023.1|AF232023	Tamandua tetradactyla clone 7 cytoch...	46	3e-04
gb|AF232022.1|AF232022	Tamandua tetradactyla clone 6 mitoch...	46	3e-04
gb|AF232021.1|AF232021	Tamandua tetradactyla clone 5 cytoch...	46	3e-04
gb|AF157466.1|AF157466	Lepus timidus cytochrome b (Cyb) gen...	46	3e-04
gb|AF157465.1|AF157465	Lepus granatensis cytochrome b (Cyb)...	46	3e-04
gb|AF157464.1|AF157464	Lepus corsicanus haplotype 1 cytochr...	46	3e-04
gb|AF157463.1|AF157463	Lepus corsicanus haplotype 3 cytochr...	46	3e-04
gb|AF157460.1|AF157460	Lepus europaeus cytochrome b (Cyb) g...	46	3e-04
gb|AF231664.1|AF231664	Tylosurus crocodilus crocodilus cyto...	46	3e-04
gb|AF231663.1|AF231663	Tylosurus crocodilus clone STRI-3537...	46	3e-04
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AF158692	398	422
AF068192	401	425

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AB021091	398	....	422

AB001612	398	....	422
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D32192	398	....	422
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AJ010048	269	....	293
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AF157463	324	....	346
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    Posted date:  Mar 2, 2001 12:20 AM
  Number of letters in database: 2,863,827,885
  Number of sequences in database:  807,597

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    1.37    0.711     1.31

Gapped
Lambda     K      H
    1.37    0.711     1.31


Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 39355
Number of Sequences: 807597
Number of extensions: 39355
Number of successful extensions: 15066
Number of sequences better than 10.0: 5706
length of query: 25
length of database: 2,863,827,885
effective HSP length: 17
effective length of query: 8
effective length of database: 2,850,098,736
effective search space: 22800789888
effective search space used: 22800789888
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A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 16 (32.2 bits)
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Table 11. BLAST analysis of primers 'mcb869' in *nr* database of NCBI. It demonstrates that the 3' end of this primer is highly conserved among a vast range of animal species. It also shows the significant homology among the primer and templates (i.e. the cytochrome b gene fragment of different animal species), confirming the universal nature of our primer.

BLASTN 2.1.2 [Nov-13-2000]

Reference:
Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 984593033-24247-14777

Query=
(26 letters)

Database: nt
807,597 sequences; 2,863,827,885 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

Distribution of 500 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Sequences producing significant alignments:

		Score (bits)	E Value
gb|AF189111.1|AF189111	Cryptotermes austrinus cytochrome b ...	52	6e-06
gb|U86834.1|U86834	Phyllotis wolffsohni MSB 67270 cytochrom...	52	6e-06
gb|AF123633.1|AF123633	Perissocephalus tricolor cytochrome ...	52	6e-06
gb|AF123617.1|AF123617	Pipreola arcuata cytochrome b gene, ...	52	6e-06
gb|AF127202.1|AF127202	Hylopezus fulviventris cytochrome b ...	52	6e-06
gb|AF127194.1|AF127194	Grallaria guatimalensis cytochrome b...	52	6e-06
gb|AF217828.1|AF217828	Aspidelaps scutatus cytochrome b gen...	52	6e-06
gb|AF160578.1|AF160578	Hypogeomys antimena Hant555 cytochro...	52	6e-06
gb|AF009931.2|AF009931	Archocentrus centrarchus cytochrome ...	52	6e-06
gb|AF091629.1|AF091629	Antilocapra americana cytochrome b (...	52	6e-06
gb|AF034967.1|	Sigmoceros lichtensteinii cytochrome b gene,...	52	6e-06
gb|AF038290.1|AF038290	Antechinus sp. cytochrome b gene, mi...	52	6e-06
gb|U07577.1|AMU07577	Antechinus melanurus mitochondrion cyt...	52	6e-06
gb|U81343.1|CFU81343	Chelus fimbriata cytochrome b gene, mi...	52	6e-06
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gb|M99464.1|PNZMTCYTB	Planigale sp. cytochrome b gene, comp...	52	6e-06
emb|AJ225116.1|DNJ225116	Dryomys nitedula mitochondrial gen...	52	6e-06
gb|U25738.1|PRU25738	Paradisaea raggiana cytochrome b gene,...	52	6e-06
gb|U25736.1|PRU25736	Paradisaea rubra cytochrome b gene, mi...	52	6e-06
gb|U15202.1|SMU15202	Seleucidis melanoleuca mitochondrion c...	52	6e-06
gb|U15204.1|PR15204	Paradisaea raggiana mitochondrion cytoc...	52	6e-06
emb|X56290.1|MIDDCYTB	D.dama mitochondrion cytb gene for cy...	52	6e-06
emb|X56286.1|MIAACYTBA	A.americana mitochondrion cytb gene ...	52	6e-06
dbj|D88639.1|D88639	Anoa depressicornis mitochondrial DNA f...	52	6e-06
dbj|D82890.1|D82890	Bubalus depressicornis mitochondrial DN...	52	6e-06
gb|AF119261.1|AF119261	Peromyscus maniculatus cytochrome b ...	46	3e-04
gb|AF123615.1|AF123615	Rupicola rupicola cytochrome b gene,...	46	3e-04
gb|AF160603.1|AF160603	Apodemus sylvaticus Asyl588 cytochro...	46	3e-04
gb|U62687.1|CCOLCYTB2	Charadrius collaris cytochrome b (cyt...	46	3e-04
gb|U62685.1|CBICCYTB2	Charadrius bicinctus cytochrome b (cy...	46	3e-04
gb|AF022071.1|	Madoqua guentheri cytochrome b (cytb) gene, ...	46	3e-04
gb|AF022070.1|	Madoqua kirkii cytochrome b (cytb) gene, mit...	46	3e-04
gb|U83317.1|PSU83317	Polihierax semitorquatus cytochrome b ...	46	3e-04
gb|U37293.1|CCU37293	Cepphus columba cytochrome b gene, mit...	46	3e-04
gb|U37292.1|CCU37292	Cepphus carbo cytochrome b gene, mitoc...	46	3e-04
gb|U37291.1|BMU37291	Brachyramphus marmoratus perdix cytoch...	46	3e-04
gb|AF082055.1|AF082055	Rupicola rupicola cytochrome b gene,...	46	3e-04
gb|U72770.1|JMU72770	Jabiru mycteria cytochrome b gene, mit...	46	3e-04
gb|U07578.1|DCU07578	Dasycercus cristicauda mitochondrion c...	46	3e-04
gb|AF031908.1|GOCCCYTB1	Geopsittacus occidentalis cytochrom...	46	3e-04
emb|AJ004231.1|SBAJ4231	Sula bassana mitochondrial cytb gen...	46	3e-04
emb|AJ004230.1|SBAJ4230	Sula bassana mitochondrial cytb gen...	46	3e-04
emb|AJ004229.1|SBAJ4229	Sula bassana mitochondrial cytb gen...	46	3e-04
emb|AJ004232.1|SBAJ4232	Sula bassana mitochondrial cytb gen...	46	3e-04
gb|U88865.1|	Pomacentrus sp. cytochrome b (cytb) gene, mito...	46	3e-04
gb|U90001.1|MBU90001	Morus bassanus cytochrome b gene, mito...	46	3e-04
gb|U63057.1|BMU63057	Brachyramphus marmoratus perdix cytoch...	46	3e-04
dbj|AB036404.1|AB036404	Rana porosa brevipoda mitochondrial...	46	3e-04
dbj|AB036402.1|AB036402	Rana porosa brevipoda mitochondrial...	46	3e-04
dbj|AB036400.1|AB036400	Rana porosa brevipoda mitochondrial...	46	3e-04
dbj|AB036398.1|AB036398	Rana porosa porosa mitochondrial DN...	46	3e-04
gb|U19611.1|JMU19611	Jabiru mycteria cytochrome b gene, mit...	46	3e-04
emb|X92539.1|HACYTB	H.ampullatus cytochrome b gene (complet...	46	3e-04
gb|L08034.1|GAEMTCYTBA	Galeocerdo cuvier mitochondrial cyto...	46	3e-04
gb|L08033.1|CPLMTCYTBB	Carcharhinus porosus mitochondrial c...	46	3e-04
gb|AY016012.1|	Crypturellus tataupa mitochondrion, partial ...	44	0.001
gb|AF074591.1|AF074591	Petrochelidon pyrrhonota cytochrome ...	44	0.001
gb|AY005212.1|	Poospiza whitii isolate 2 cytochrome b (cytb...	44	0.001
gb|AY005211.1|	Poospiza whitii isolate 1 cytochrome b (cytb...	44	0.001
gb|AF189122.1|AF189122	Cryptotermes tropicalis cytochrome b...	44	0.001
gb|AF189120.1|AF189120	Cryptotermes secundus cytochrome b (...	44	0.001
gb|AF189119.1|AF189118	Cryptotermes primus isolate 2 cytoch...	44	0.001
gb|AF189117.1|AF189117	Cryptotermes primus isolate 1 cytoch...	44	0.001
gb|AF189115.1|AF189115	Cryptotermes dudleyi cytochrome b (Cy...	44	0.001
gb|AF112149.1|AF112149	Ovis canadensis cytochrome b gene, p ...	44	0.001
gb|AF112132.1|AF112132	Ovis canadensis canadensis cytochrom...	44	0.001
gb|AF112135.1|AF112135	Ovis canadensis nelsoni cytochrome b .	44	0.001
gb|AF291229.1|AF291229	Vireo cassinii cassinii specimen-vou	44	0.001

gb|AF081989.1|AF081989	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081988.1|AF081988	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081987.1|AF081987	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081986.1|AF081986	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081985.1|AF081985	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081984.1|AF081984	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081983.1|AF081983	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081982.1|AF081982	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081981.1|AF081981	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081980.1|AF081980	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081979.1|AF081979	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081978.1|AF081978	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081977.1|AF081977	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081976.1|AF081976	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081975.1|AF081975	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081974.1|AF081974	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081973.1|AF081973	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081972.1|AF081972	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081971.1|AF081971	Vireo cassinii cassinii specimen-vou...	44	0.001
gb|AF081970.1|AF081970	Vireo solitarius alticola country US...	44	0.001
gb|AF081969.1|AF081969	Vireo solitarius alticola country US...	44	0.001
gb|AF081968.1|AF081968	Vireo solitarius alticola country US...	44	0.001
gb|AF081967.1|AF081967	Vireo solitarius alticola country US...	44	0.001
gb|AF081966.1|AF081966	Vireo solitarius solitarius specimen...	44	0.001
gb|AF081965.1|AF081965	Vireo solitarius solitarius specimen...	44	0.001
gb|AF081964.1|AF081964	Vireo solitarius solitarius specimen...	44	0.001
gb|AF081962.1|AF081962	Vireo flavifrons specimen-voucher LS...	44	0.001
gb|AF081961.1|AF081961	Vireo flavifrons specimen-voucher LS...	44	0.001
gb|AF081960.1|AF081960	Vireo leucophrys leucophrys specimen...	44	0.001
gb|AF081959.1|AF081959	Vireolanius leucotis leucotis cytoch...	44	0.001
gb|AF112405.2|AF112405	Barbus anoplus cytochrome b (cytb) g...	44	0.001
gb|AF144317.1|AF144317	Amphiprion ocellaris isolate 3 haplo...	44	0.001
gb|AF144316.1|AF144316	Amphiprion ocellaris haplotype 3DH11...	44	0.001
gb|AF144315.1|AF144315	Amphiprion ocellaris haplotype 3DH15...	44	0.001
gb|AF144314.1|AF144314	Amphiprion ocellaris isolate 2 haplo...	44	0.001
gb|AF144313.1|AF144313	Amphiprion ocellaris isolate 1 haplo...	44	0.001
gb|AF144312.1|AF144312	Amphiprion ocellaris haplotype 3DH12...	44	0.001
gb|AF144311.1|AF144311	Amphiprion ocellaris haplotype 3DH1 ...	44	0.001
gb|AF144310.1|AF144310	Amphiprion ocellaris isolate 2 haplo...	44	0.001
gb|AF144309.1|AF144309	Amphiprion ocellaris isolate 1 haplo...	44	0.001
ref|NC_001567.1|	Bos taurus mitochondrion, complete genome	44	0.001
gb|AF212124.1|AF212124	Anolis schwartzi cytochrome b gene, ...	44	0.001
gb|AF182706.1|AF182706	Phapitreron amethystina cytochrome b:..	44	0.001
gb|AF010406.1|AF010406	Ovis aries complete mitochondrial ge...	44	0.001
gb|AF096452.1|AF096452	Platysteira cyanea cytochrome b gene...	44	0.001
gb|AF283619.1|AF283619	Elaphe obsoleta LSUMZ39162 cytochrom...	44	0.001
gb|AF283618.1|AF283618	Elaphe obsoleta LSUMZ H15896 cytochr...	44	0.001
gb|AF283608.1|AF283608	Elaphe obsoleta LSUMZ H14782 cytochr...	44	0.001
gb|AF283602.1|AF283602	Elaphe obsoleta LSUMZ H3388 cytochro...	44	0.001
gb|AF310069.1|AF310069	Elaenia martinica cytochrome b gene,...	44	0.001
gb|AF146616.1|AF146616	Actophilornis africanus cytochrome b...	44	0.001
gb|AF271410.1|AF271410	Galago moholi cytochrome b (cyt b) g...	44	0.001
gb|AF290139.1|AF290139	Peucedramus taeniatus cytochrome b (...	44	0.001
ref|NC_002504.1|	Lama pacos mitochondrion, complete genome	44	0.001
gb|AF163901.1|AF163901	Microtus ochrogaster cytochrome b ge...	44	0.001
gb|AF119263.1|AF119263	Myopus schisticolor cytochrome b gen...	44	0.001
gb|AF119259.1|AF119259	Synaptomys borealis cytochrome b gen...	44	0.001
gb|AF288454.1|AF288454	Nyctereutes procyonoides koreensis c...	44	0.001
gb|AF163895.1|AF163895	Microtus gregalis cytochrome B (cytB...	44	0.001
gb|AF123649.1|AF123649	Machaeropterus regulus striolatus cy...	44	0.001
gb|AF123647.1|AF123647	Machaeropterus pyrocephalus cytochro...	44	0.001
gb|AF123646.1|AF123646	Xenopipo atronitens cytochrome b gen...	44	0.001
gb|AF123645.1|AF123645	Pipra fasciicauda cytochrome b gene,...	44	0.001
gb|AF123634.1|AF123634	Pyroderus scutatus cytochrome b gene...	44	0.001
gb|AF123632.1|AF123632	Cephalopterus ornatus cytochrome b g...	44	0.001
gb|AF123628.1|AF123628	Turdampelis cryptolophus cytochrome ...	44	0.001
gb|AF123621.1|AF123621	Porphyrolaema porphyrolaema cytochro...	44	0.001
gb|AF123619.1|AF123619	Ampelioides tschudii cytochrome b ge...	44	0.001
gb|AF123618.1|AF123618	Pipreola chlorolepidota cytochrome b...	44	0.001
gb|AF123614.1|AF123614	Rupicola peruviana cytochrome b gene...	44	0.001
gb|AF123611.1|AF123611	Doliornis sclateri cytochrome b gene ...	44	0.001

gb|AF127201.1|AF127201	Myrmothera campanisona cytochrome b ...	44	0.001
gb|AF127192.1|AF127192	Grallaria ruficapilla cytochrome b g...	44	0.001
gb|AF127189.1|AF127189	Grallaria varia cytochrome b gene, p...	44	0.001
gb|AF197849.1|AF197849	Sericornis frontalis cytochrome b ge...	44	0.001
gb|AF197847.1|AF197847	Pardalotus striatus cytochrome b gen...	44	0.001
ref|NC 000889.1|	Hippopotamus amphibius mitochondrion, comp...	44	0.001
ref|NC 002079.1|	Carassius auratus mitochondrion, complete ...	44	0.001
ref|NC 001794.1|	Macropus robustus mitochondrion, complete ...	44	0.001
ref|NC 001610.1|	Didelphis virginiana mitochondrion, comple...	44	0.001
gb|AF201612.1|AF201612	Stomatorhinus sp. CU79703 cytochrome...	44	0.001
gb|AF097931.1|AF097931	Amphiprion clarkii cytochrome b gene...	44	0.001
gb|AF097927.1|AF097927	Amphiprion ocellaris cytochrome b ge...	44	0.001
gb|J01394.1|BOVMT	Bos taurus mitochondrion, complete genome	44	0.001
gb|AF168760.1|AF168760	Apalone spinifera isolate TXsc cytoc...	44	0.001
gb|AF168759.1|AF168759	Apalone spinifera isolate TXki cytoc...	44	0.001
gb|AF168758.1|AF168758	Apalone spinifera isolate TXcc cytoc...	44	0.001
gb|AF168756.1|AF168756	Apalone spinifera isolate NMrg cytoc...	44	0.001
gb|AF182381.1|AF182381	Petrochelidon rufocollaris isolate E...	44	0.001
gb|AF182380.1|AF182380	Petrochelidon rufocollaris isolate E...	44	0.001
gb|U89187.1|MMU89187	Momotus mexicanus cytochrome b (cytb) ...	44	0.001
gb|AF193833.1|AF193833	Botaurus lentiginosus cytochrome b g...	44	0.001
gb|AF193822.1|AF193822	Ardea alba cytochrome b gene, partia...	44	0.001
gb|AF193821.1|AF193821	Ardea herodias cytochrome b gene, pa...	44	0.001
gb|AF217837.1|AF217837	Paranaja multifasciata cytochrome b ...	44	0.001
gb|AF217835.1|AF217835	Naja kaouthia cytochrome b gene, com...	44	0.001
gb|AF217834.1|AF217834	Laticauda colubrina cytochrome b gen...	44	0.001
gb|AF217831.1|AF217831	Calliophis japonicus cytochrome b ge...	44	0.001
gb|AF217823.1|AF217823	Micruroides euryxanthus cytochrome b...	44	0.001
gb|AF217819.1|AF217819	Drysdalia coronata cytochrome b gene...	44	0.001
gb|AF217815.1|AF217815	Austrelaps superbus cytochrome b gen...	44	0.001
gb|AF118156.1|AF118156	Terenura humeralis specimen-voucher ...	44	0.001
gb|AF209938.1|AF209938	Euura atra isolate 62 cytochrome b g...	44	0.001
gb|AF209933.1|AF209933	Euura atra isolate C cytochrome b ge...	44	0.001
gb|AF059104.1|AF059104	Marmaronetta angustirostris cytochro...	44	0.001
gb|AF059102.1|AF059102	Lophonetta specularoides cytochrome ...	44	0.001
gb|AF059054.1|AF059054	Amazonetta brasiliensis cytochrome b...	44	0.001
gb|AF192646.1|AF192646	Hippocampus barbouri haplotype PH.22...	44	0.001
gb|AF192645.1|AF192645	Hippocampus barbouri haplotype PH.13...	44	0.001
gb|AF160614.1|AF160614	Cricetomys gambianus Cgam518 cytochr...	44	0.001
gb|AF160613.1|AF160613	Cricetomys emini Cemi531 cytochrome ...	44	0.001
gb|AF160612.1|AF160612	Cricetomys emini Cemi530 cytochrome ...	44	0.001
gb|AF160611.1|AF160611	Cricetomys emini Cemi637 cytochrome ...	44	0.001
gb|AF160610.1|AF160610	Cricetomys emini Cemi636 cytochrome ...	44	0.001
gb|AF160604.1|AF160604	Calomyscus bailwardi Cbal576 cytochr...	44	0.001
gb|AF160560.1|AF160560	Eliurus majori Emaj642 cytochrome b ...	44	0.001
gb|AF160559.1|AF160559	Eliurus majori Emaj641 cytochrome b ...	44	0.001
gb|AF160558.1|AF160558	Eliurus majori Emaj639 cytochrome b ...	44	0.001
gb|AF160557.1|AF160557	Eliurus majori Emaj638 cytochrome b ...	44	0.001
gb|AF160555.1|AF160555	Eliurus majori Emaj614 cytochrome b ...	44	0.001
gb|AF160554.1|AF160554	Eliurus majori Emaj617 cytochrome b ...	44	0.001
gb|AF160553.1|AF160553	Eliurus majori Emaj573 cytochrome b ...	44	0.001
gb|AF160552.1|AF160552	Eliurus majori Emaj556 cytochrome b ...	44	0.001
gb|AF160551.1|AF160551	Eliurus majori Emaj561 cytochrome b ...	44	0.001
gb|AF160550.1|AF160550	Eliurus majori Emaj443 cytochrome b ...	44	0.001
gb|AF160549.1|AF160549	Eliurus majori Emaj444 cytochrome b ...	44	0.001
gb|AF036287.1|AF036287	Damaliscus pygargus cytochrome b (cy...	44	0.001
gb|AF036286.1|AF036286	Oryx leucoryx cytochrome b (cytb) ge...	44	0.001
gb|AF036283.1|AF036283	Antilope cervicapra cytochrome b (cy...	44	0.001
gb|AF036281.1|AF036281	Antidorcas marsupialis cytochrome b ...	44	0.001
gb|AF036278.1|AF036278	Tragelaphus oryx cytochrome b (cytb)...	44	0.001
gb|AF036276.1|AF036276	Tragelaphus eurycerος cytochrome b (...	44	0.001
gb|AF036274.1|	Tetracerus quadricornis cytochrome b (cytb) ...	44	0.001
ref|NC 001941.1|	Ovis aries mitochondrion, complete genome	44	0.001
gb|AF108698.1|AF108698	Microryzomys minutus cytochrome B (c...	44	0.001
gb|AF108682.1|AF108682	Rhipidomys nitela cytochrome B (cytB...	44	0.001
gb|AF108673.1|AF108673	Thomasomys daphne cytochrome B (cytB...	44	0.001
gb|AF108662.1|AF108662	Scapteromys tumidus cytochrome B (cy...	44	0.001
gb|AF042720.1|AF042720	Megamuntiacus vuquangensis cytochrom...	44	0.001
gb|AF042719.1|	Muntiacus muntjak cytochrome b gene, mitocho...	44	0.001
gb|AF084083.1|AF084083	Stenella coeruleoalba cytochrome b g...	44	0.001
gb|AF084081.1|AF084081	Stenella coeruleoalba cytochrome b g ...	44	0.001

gb|AF084074.1|AF084074	Lagenorhynchus albirostris cytochrom...	44	0.001
gb|AF090750.1|AF090750	Gobio gobio balcanicus cytochrome b ...	44	0.001
gb|AF157939.1|AF157939	Spermophilus columbianus columbianus...	44	0.001
gb|AF157937.1|AF157937	Spermophilus washingtoni isolate S89...	44	0.001
gb|AF157936.1|AF157936	Spermophilus washingtoni isolate S88...	44	0.001
gb|AF157915.1|AF157915	Spermophilus richardsoni isolate S63...	44	0.001
gb|AF157914.1|AF157914	Spermophilus richardsoni isolate S62...	44	0.001
gb|AF157912.1|AF157912	Spermophilus undulatus isolate S60 c...	44	0.001
gb|AF157906.1|AF157906	Spermophilus undulatus isolate S55 c...	44	0.001
gb|AF157891.1|AF157891	Spermophilus elegans elegans isolate...	44	0.001
gb|AF157882.1|AF157882	Spermophilus columbianus columbianus...	44	0.001
gb|AF157859.1|AF157859	Spermophilus citellus isolate S118 c...	44	0.001
gb|AF157858.1|AF157858	Spermophilus citellus isolate S117 c...	44	0.001
gb|AF157839.1|AF157839	Spermophilus elegans elegans isolate...	44	0.001
gb|AF030497.1|AF030497	Crocidura brunnea cytochrome b (cyt ...	44	0.001
gb|U03541.2|LAU03541	Lenoxus apicalis cytochrome b gene, pa...	44	0.001
gb|AF009951.2|AF009951	Heros appendiculatus cytochrome b (c...	44	0.001
gb|AF009941.1|AF009941	Tomocichla tuba cytochrome b (cytb) ...	44	0.001
gb|AF009925.1|AF009925	Archocentrus sajica cytochrome b (cy...	44	0.001
gb|AF094633.1|AF094633	Stachyris whiteheadi cytochrome b ge...	44	0.001
gb|AF094621.1|AF094621	Eminia lepida cytochrome b gene, par...	44	0.001
gb|AF094618.1|AF094618	Hypergerus atriceps cytochrome b gen...	44	0.001
gb|AF166348.1|AF166348	Phascolarctos cinereus cytochrome b ...	44	0.001
gb|AF158697.1|AF158697	Geomys bursarius ozarkensis cytochro...	44	0.001
gb|AF158694.1|AF158694	Geomys bursarius majusculus cytochro...	44	0.001
gb|AF158693.1|AF158693	Geomys bursarius bursarius cytochrom...	44	0.001
gb|AF158688.1|AF158688	Geomys bursarius missouriensis cytoc...	44	0.001
gb|AF100720.1|AF100720	Spermophilus citellus cytochrome b (...	44	0.001
gb|AF091632.1|AF091632	Bubalus depressicornis cytochrome b ...	44	0.001
gb|AF102815.1|AF102815	Dromiciops gliroides cytochrome b ge...	44	0.001
gb|AF102814.1|AF102814	Vombatus ursinus cytochrome b gene, ...	44	0.001
gb|AF022065.1|	Tragelaphus euryceros cytochrome b (cytb) ge...	44	0.001
gb|AF022059.1|	Kobus ellipsiprymnus cytochrome b (cytb) gen...	44	0.001
gb|AF022058.1|	Antilope cervicapra cytochrome b (cytb) gene...	44	0.001
gb|AF022057.1|	Tragelaphus oryx cytochrome b (cytb) gene, m...	44	0.001
gb|AF022054.1|	Antidorcas marsupialis cytochrome b (cytb) g...	44	0.001
gb|AF016637.1|AF016637	Connochaetes gnou cytochrome b (cytb...	44	0.001
gb|U69863.1|PSU69863	Python sebae cytochrome b (cytb) gene,...	44	0.001
gb|U69844.1|LTU69844	Lichanura trivirgata cytochrome b (cyt...	44	0.001
gb|AF143193.1|AF143193	Epinephelus sp. cytochrome b (cytb) ...	44	0.001
gb|AF121222.1|AF121222	Amphiprion ocellaris isolate 8 cytoc...	44	0.001
gb|AF096625.1|AF096625	Kobus ellipsiprymnus defassa cytochr...	44	0.001
gb|AF096624.1|AF096624	Kobus ellipsiprymnus ellipsiprymus c...	44	0.001
gb|AF081052.1|AF081052	Eulemur rubriventer cytochrome b (cy...	44	0.001
gb|AF081049.1|AF081049	Eulemur macaco macaco cytochrome b (...	44	0.001
gb|AF081048.1|AF081048	Eulemur fulvus albifrons cytochrome ...	44	0.001
gb|AF082063.1|AF082063	Elminia longicauda cytochrome b gene...	44	0.001
emb|AJ010957.1|HAAJ10957	Hippopotamus amphibius complete mi...	44	0.001
gb|U76506.1|CLU76506	Chlamydera lauterbachii cytochrome b g...	44	0.001
gb|U76504.1|CCU76504	Chlamydera cerviniventris cytochrome b...	44	0.001
gb|U76505.1|ASU76505	Amblyornis subalaris cytochrome b gene...	44	0.001
gb|U76503.1|APU76503	Archboldia papuensis cytochrome b gene...	44	0.001
gb|U76508.1|AIU76508	Amblyornis inornatus cytochrome b gene...	44	0.001
gb|AF034969.1|AF034969	Connochaetes taurinus cytochrome b g...	44	0.001
gb|AF051876.1|AF051876	Rhodeus ocellatus cytochrome b (cytb...	44	0.001
gb|AF082007.1|AF082007	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF082006.1|AF082006	Vireo plumbeus plumbeus specimen-vou...	44	0.001
gb|AF082005.1|AF082005	Vireo plumbeus plumbeus specimen-vou...	44	0.001
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gb|U53580.1|NCU53580	Nycticebus coucang cytochrome b (cyt b...	44	0.001
gb|U53577.1|EFU53577	Eulemur fulvus rufus cytochrome b (cyt...	44	0.001
gb|U53576.1|EFU53576	Eulemur fulvus collaris cytochrome b (...	44	0.001
gb|U95512.1|ESERCYTB2	Eptesicus serotinus 3' cytochrome b (...	44	0.001
gb|U95508.1|PKUHLCYTB2	Pipistrellus kuhli 5' cytochrome b (...	44	0.001
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gb|U17867.1|BTU17867	Budorcas taxicolor bedfordi cytochrome...	44	0.001
gb|U17860.1|ODU17860	Ovis dalli cytochrome b gene, mitochon...	44	0.001
gb|U17859.1|OCU17859	Ovis canadensis cytochrome b gene, mit...	44	0.001
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gb|AF038284.1|AF038284	Antechinus swainsonii cytochrome b g...	44	0.001
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emb|AJ222685.1|ODCYTOB	Oryx dammah mitochondrial cytochrome...	44	0.001
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gb|M99450.1|DAVMTCYTB	Dasyurus hallucatus cytochrome b gene...	44	0.001
gb|U25737.1|PMU25737	Paradisaea minor cytochrome b gene, mi...	44	0.001
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emb|AJ000427.1|SAAJ427	Sorex arcticus ssp. maritimensis par...	44	0.001
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emb|AJ004792.1|HCAJ4792	Hippolais caligata ssp. rama mitoch...	44	0.001
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gb|U34679.1|POU34679	Philander opossum cytochrome b light s...	44	0.001
gb|L11907.1|CGYMTCYTBF	Cratogeomys goldmani rubellus mitoch...	44	0.001
gb|L11906.1|CGYMTCYTBE	Cratogeomys merriami mitochondrial c...	44	0.001
gb|L11902.1|CGYMTCYTBA	Cratogeomys castanops castanops mito...	44	0.001
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emb|X74260.1|MIVOCYTB	V.olivaceus mitochondrion gene for cy...	44	0.001
emb|X56293.1|MISLCYTBB	S.longiroshis mitochondrion cytb gen...	44	0.001
emb|X56292.1|MISLCYTBA	S.longirostris mitochondrion cytb ge...	44	0.001
emb|X74256.1|MIPVCYTB	P.violaceus mitochondrion gene for cy...	44	0.001
emb|X82304.1|MIPHCYTBG	P.hispida mitochondrial cytochrome b...	44	0.001
emb|X82302.1|MIPFCYTBG	P.fasciata mitochondrial cytochrome ...	44	0.001
emb|X56284.1|MIOACYTB	O.aries mitochondrion cytb gene for c...	44	0.001
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emb|X74259.1|MILLCYTB	L.ludovicianus mitochondrion gene for...	44	0.001
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emb|X56289.1|MICHCYTB	C.hircus mitochondrion cytb gene for ...	44	0.001
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dbj|D34637.1|BBUMTCBA	Bubalus bubalis mitochondrial gene fo...	44	0.001
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dbj|D88629.1|D88629	Bubalus bubalis mitochondrial DNA for c...	44	0.001
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gb|U10367.1|PVU10367	Ptilonorhynchus violaceus mitochondrio...	44	0.001
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gb|AF157463.1|AF157463	Lepus corsicanus haplotype 3 cytochr...	40	0.021
gb|AY016019.1|AY016018S3	Mulleromis agilis cytochrome b ge...	40	0.021
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emb|AJ004315.1|HCAJ4315	Hippolais caligata mitochondrial cy...	38	0.084

Alignments

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AF123617   104    .......................... 79
AF127202   107    .......................... 82
AF127194   107    .......................... 82
AF217828   845    .......................... 820
AF160578   869    .......................... 844
AF009931   869    .......................... 844
AF091629   869    .......................... 844
AF034967   869    .......................... 844
AF038290   869    .......................... 844
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U81343     791    .......................... 766
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M99464     869    .......................... 844
AJ225116   869    .......................... 844
U25738     872    .......................... 847
U25736     872    .......................... 847
U15202     872    .......................... 847
U15204     872    .......................... 847
X56290     869    .......................... 844
X56286     869    .......................... 844
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D82890     869    .......................... 844
AF119261   869    .......................    847
AF123615   101       ....................... 79
AF160603   866       ....................... 844
U62687     179    .......................    157
U62685     179    .......................    157
AF022071   866       ....................... 844
AF022070   866       ....................... 844
U83317     872    .......................    850
U37293     774    .......................    752
U37292     774    .......................    752
U37291     774    .......................    752
AF082055   51        ....................... 29
U72770     798    .......................    776
U07578     869    .......................    847
AF031908   187    .......................    165
AJ004231   773    .......................    751
AJ004230   773    .......................    751
AJ004229   773    .......................    751
AJ004232   773    .......................    751
U88865     850    .......................    828
U90001     536    .......................    514
U63057     773    .......................    751
AB036404   173    .......................    151
AB036402   173    .......................    151
AB036400   173    .......................    151
AB036398   173    .......................    151
U19611     774    .......................    752
X92519     869    .......................    847
L08034     872    .......................    850
L08031     872    .......................    850
AX016012   11937  ....................a..... 11912
AF074591   677    ..............t........... 652
AX005212   761    ....................g..... 736
AX005211   761    ....................g..... 736
AF182122   797    .....c.................... 772
AF182120   797    ..............t........... 772
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AF189116	797	..............g...........	772
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AF112139	310	..............g...........	285
AF112138	310	..............g...........	285
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AF081989	872	..............t...........	847
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AF081965	872	..............t...........	847
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AF081962	754	..............t...........	729
AF081961	872	..............t...........	847
AF081960	872	..............g...........	847
AF081959	872	..............t...........	847
AF112405	869	....................c.....	844
AF144317	161	....................g.....	136
AF144316	161	....................g.....	136
AF144315	161	....................g.....	136
AF144314	161	....................g.....	136
AF144313	161	....................g.....	136
AF144312	161	....................g.....	136
AF144311	161	....................g.....	136
AF144310	161	....................g.....	136
AF144309	161	....................g.....	136
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AF283608	845	...........a..............	820
AF283602	845	...........a..............	820
AF310069	770	.................a........	745
AF146616	95	..............g...........	70
AF271410	869	..............g...........	844
AF290139	752	....................g.....	727
NC_002504	15022	..............g...........	14997
AF161901	869	....................g.....	844
AF119261	869	..............g...........	844
AF119259	869	....................g.....	844
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AF121647	68	..............g...........	43
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AF121645	68	..............g...........	43
AF121634	84	..............g...........	59

[illegible]	[illegible]	.....c....................	79
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AF123621	85	....................g.....	60
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AF123618	104	....................g.....	79
AF123614	104	..............g...........	79
AF123613	101	..............g...........	76
AF127201	107	..............g...........	82
AF127192	107	..............t...........	82
AF127189	107	..............g...........	82
AF197849	872	....................g.....	847
AF197847	872	..............t...........	847
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AF097927	869	....................g.....	844
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AF168759	507	....................a.....	482
AF168758	507	....................a.....	482
AF168756	507	....................a.....	482
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AF182380	692	..............t...........	667
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AF193821	773	....................a.....	748
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AF217819	845	.....a....................	820
AF217815	845	..............c...........	820
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AF209933	418	...........a..............	393
AF059104	776	.....c....................	751
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AF059054	776	..............c...........	751
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AF160611	238	....................g.....	213
AF160610	869	....................g.....	844
AF160604	869	....................g.....	844
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AF160559	869	....................a.....	844
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AF160552	869	....................a.....	844
AF160551	869	....................a.....	844
AF160550	869	....................a.....	844
AF160549	869	....................a.....	844
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AF016286	869	..............g...........	844
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AF016281	869	.................a........	844
AF016278	869	..............g...........	844
AF016276	867	...........a..............	844
AF016274	869	..............g...........	844
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AF108682	869	....................a.....	844
AF108673	869	....................g.....	844
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AF042718	869	.................a........	844
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AF084081	869	.....a....................	844
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AF157937	869	....................a.....	844
AF157936	869	....................a.....	844
AF157915	869	....................a.....	844
AF157914	869	....................a.....	844
AF157912	869	....................g.....	844
AF157906	869	....................g.....	844
AF157891	869	....................g.....	844
AF157882	869	....................a.....	844
AF157859	869	....................a.....	844
AF157858	869	....................a.....	844
AF157839	869	....................g.....	844
AF030497	50	.....a....................	25
U03541	869	....................g.....	844
AF009951	866	.................a........	841
AF009941	869	..............g...........	844
AF009925	869	.................a........	844
AF094633	737	....................g.....	712
AF094621	737	..............t...........	712
AF094618	737	..............t...........	712
AF166348	869	..............g...........	844
AF158697	869	...........a..............	844
AF158694	869	...........a..............	844
AF158693	869	...........a..............	844
AF158688	869	...........a..............	844
AF100720	869	....................a.....	844
AF091632	869	.................a........	844
AF102815	869	....................a.....	844
AF102814	869	..............t...........	844
AF022065	869	...........a..............	844
AF022059	869	..............g...........	844
AF022058	869	.................a........	844
AF022057	869	..............g...........	844
AF022054	869	.................a........	844
AF016637	869	..........c...............	844
U69863	845	..............t...........	820
U69844	845	..............t...........	820
AF143193	869	....................a.....	844
AF121222	140	....................g.....	115
AF096625	869	..............g...........	844
AF096624	869	..............g...........	844
AF081052	869	....................a.....	844
AF081049	869	....................a.....	844
AF081048	869	....................g.....	844
AF082063	54	....................g.....	29
AJ010957	15040	..............g...........	15015
U76506	773	..............g...........	748
U76504	773	..............g...........	748
U76505	773	..............t...........	748
U76503	773	..............t...........	748
U76508	773	..............t...........	748
AF034969	869	..............g...........	844
AF051876	869	..............t...........	844
AF082007	872	..............t...........	847
AF082006	872	..............t...........	847
AF082005	872	..............t...........	847
AF082004	872	..............t...........	847
AF082003	872	..............t...........	847
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AF081991	872	..............t...........	847
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AF012235	860	....................a.....	835
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U53577	869	....................g.....	844
U53576	869	....................a.....	844
U95512	31	....................g.....	6
U95508	31	...........a..............	6
U17868	869	..............g...........	844
U17867	869	..............g...........	844
U17860	869	..............g...........	844
U17859	800	..............g...........	775
AJ010556	869	....................g.....	844
AF034736	869	..............g...........	844
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AF034729	869	...........a..............	844
AF034728	869	..............g...........	844
AF034727	869	...........a..............	844
AF034724	869	..............g...........	844
AF034722	869	..............g...........	844
U72038	869	..............g...........	844
U72037	869	..............g...........	844
M99455	869	...........a..............	844
L29055	260	...........a..............	235
AF082047	54	....................g.....	29
AF038286	869	..............t...........	844
AF038284	869	..............t...........	844
AF059093	776	..............t...........	751
AF059092	776	..............t...........	751
AF059091	776	..............t...........	751
AF059080	776	..............t...........	751
AF059078	776	..............t...........	751
AF052240	61	....................a.....	36
AF006240	774	..............t...........	749
AF006227	774	....................g.....	749
AF047447	41	..............g...........	16
U07576	869	..............g...........	844
AF028180	65	..............g...........	40
AF028178	69	....................g.....	44
AF028170	77	....................g.....	52
M99454	869	.................a........	844
M99453	869	..............t...........	844
U23461	869	........c.................	844
U87138	869	..............g...........	844
U07590	869	....................g.....	844
AJ004326	773	.....c....................	748
AF020255	819	....................g.....	794
Y19184	15022	..............g...........	14997
U88862	843	.................a........	818
U88859	867	..............g...........	842
U88858	843	........c.................	818
U88857	863	..............g...........	838
U88856	867	..............g...........	842
Y10524	15052	....................a.....	15027
U81157	791	..............t...........	766
U81156	791	...........a..............	766
U75354	452	.................a........	427
U77112	872	....................g.....	847
Z29571	15045	..............t...........	15020
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AJ222680	869	...........a..............	844
AJ222685	869	..............g...........	844
M99466	869	.................a........	844
M99452	869	..............c...........	844

M99460	869	....................g.....	844
U25737	872	.................a........	847
U15201	872	..............t...........	847
U15205	872	.....c....................	847
U15200	872	..............g...........	847
AJ000424	740	....................g.....	715
AJ000423	740	....................g.....	715
AJ000438	740	.................a........	715
AJ000437	740	.................a........	715
AJ000428	740	....................a.....	715
AJ000427	740	....................a.....	715
AJ000426	740	....................g.....	715
AJ000425	740	....................g.....	715
AJ000418	740	....................a.....	715
AJ000417	740	....................a.....	715
AJ000416	740	....................a.....	715
AJ004793	770	..............t...........	745
AJ004792	770	..............t...........	745
U15718	774	..............t...........	749
L11905	869	...........a..............	844
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L11907	869	...........a..............	844
L11906	869	...........a..............	844
L11902	869	...........a..............	844
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AB006953	16164	..............g...........	16139
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X74260	872	..............g...........	847
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X56292	869	.....a....................	844
X74256	872	..............g...........	847
X82304	869	....................g.....	844
X82302	869	..............g...........	844
X56284	869	...........a..............	844
X74252	872	..............g...........	847
X72005	869	....................g.....	844
X74259	872	..............g...........	847
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Y08813	869	..............g...........	844
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X74253	872	..............g...........	847
X60941	773	.....c....................	748
X74255	872	..............g...........	847
X56289	869	..............g...........	844
V00654	15382	..............g...........	15357
X60940	773	..............t...........	748
X92530	869	.....a....................	844
U09265	774	....................g.....	749
AB023906	842	....................a.....	817
AB023905	842	....................a.....	817
AB023904	842	....................a.....	817
AB023903	842	....................a.....	817
D88981	869	.................a........	844
D88638	869	.................a........	844
D88636	869	.................a........	844
D88635	869	.................a........	844
D88633	869	.................a........	844
D88632	869	.................a........	844
D88630	869	.................a........	844
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D88627	869	.................a........	844
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D84203	869	..............g...........	844
D82891	869	.................a........	844
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D82882	869	..............g...........	844
D12121	869	.................a........	844

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AB004071	869	..............g...........	844
AB004069	869	..............g...........	844
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D88637	869	.................a........	844
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D88631	869	.................a........	844
D88629	869	.................a........	844
D84205	869	...........a..............	844
D84203	869	...........a..............	844
D84201	869	..............g...........	844
D82894	869	.................a........	844
D82891	869	.................a........	844
D34638	869	.................a........	844
D34636	869	..............g...........	844
AB037602	869	...........a..............	844
AB018985	869	.................a........	844
AB004075	869	..............g...........	844
AB004073	869	..............g...........	844
AB004070	869	..............g...........	844
X92531	869	..............g...........	844
U07565	869	..............g...........	844
U10367	773	..............g...........	748
U10364	773	..............g...........	748
Z96068	869	....................g.....	844
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AF157466	791	....	772
AF157464	793	....	774
AF157463	793	....	774
AY016019	93	....	74
AF027330	869	....	850
AF027329	869	....	850
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AF027327	869	....	850
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AF027309	869	....	850
AF027308	869	....	850
AF027307	869	....	850
AF266188	371	....	352
AF324034	408	....	389
AF272639	869	....	850
AF272636	869	....	850
AF272634	869	....	850
AF272633	867	....	850
AF182711	712	....	693
AF182687	774	....	755
AF155422	869	....	850
AF155400	869	....	850
AF155385	869	....	850
AF155384	869	....	850
AF155392	869	....	850
AF155391	869	....	850
AF155390	869	....	850

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AF155589  869    ....................        850
AF155588  869    ....................        850
AF123531  771       ....................     752
AF264047  869    ....................        850
AF206531  771       ....................     752
AF192706  863          .................... 844
NC_000884 15032  ....................        15013
AF004572  869    ....................        850
AF088932  869    ....................        850
U62697    176       ....................     157
U62681    179    ....................        160
U62707    179    ..............g........n.. 154
AJ004315  773    ..............t.....n..... 748
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    Posted date:  Mar 2, 2001 12:20 AM
  Number of letters in database: 2,863,827,885
  Number of sequences in database:  807,597

Lambda     K      H
    1.37    0.711     1.31

Gapped
Lambda     K      H
    1.37    0.711     1.31


Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 19068
Number of Sequences: 807597
Number of extensions: 19068
Number of successful extensions: 7580
Number of sequences better than 10.0: 2441
length of query: 26
length of database: 2,863,827,885
effective HSP length: 17
effective length of query: 9
effective length of database: 2,850,098,736
effective search space: 25650888624
effective search space used: 25650888624
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 16 (32.2 bits)
```

Table 12. The other animals belonging to distantly related species analyzed by our primers to demonstrate its universal nature

SN.	Name of the animal
1.	Indian black buck no.1
2.	Indian black buck no 2
3	sheep
4	pig
5	dog
6	chimpanzee (chimss)
7	human (humsk)
8	Hamster
9	crocodile no1
10	crocodile no2
11	turtle no1
12	turtle no2
13	mouse
14	varanus
15	Naga-naga snake
16	Indian elephant
17	hen
18	dugong
19	lizard
20	weaver bird no1
21	weaver bird no2
22	buffalo no1
23	buffalo no 2

CLAIMS

1 Universal primers named as 'mcb 398' and 'mcb 869' capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level, said primers, having the sequences:

primers name	**Sequence (5'-3')**
mcb 398	"TACCATGAGGACAAATATCATTCTG"
mcb 869	"CCTCCTAGTTTGTTAGGGATTGATCG

2. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is capable of significantly discriminating amongst various evolutionary lineages of different animal species.
3. Primers as claimed in claim 1 wherein the fragment of mitochondrial cytochrome b gene is flanked by the highly conserved sequences amongst a vast range of animal species.
4. Primers as claimed in claim 1 wherein the fragment on mitochondrial cytochrome b gene which is polymorphic inter-specifically, but monomorphic at intra species sources.
5. Primers as claimed in claim 1 wherein in *Antilope cervicapra* species, the sequences of the fragment mentioned under claim 1 are as follows:

   Mitochondrial cytochrome b gene sequence (398-869 bp) of *Antilope cervicapra:*

   "taccatgaggacaaatatctttttgaggagcaacagtcatcaccaatctcctttcagcaatcccatacatcggtacaaacctag
   tagaatgaatctgaggagggttctcagtagataaagcaacccttacccgatttttcgccttccactttatcctcccatttatcattgc
   agcccttaccatagtacacctactgtttctccacgaaacaggatccaacaaccccacaggaatctcatcagacgcagacaaa
   attccattccacccctactacactatcaaagatatcctaggagctctactattaattttaaccctcatgcttctagtcctattctcacc
   ggacctgcttggagacccagacaactatacaccagcaaacccacttaatacacccccacatatcaagcccgaatgatacttc
   ctatttgcatacgcaatcctccgatcaattcctaacaaactaggagg"
6. A method for the identification of the animal from a biological sample, said method comprising the steps of:
   a) isolating and amplifying the DNA from the biological sample to be tested using the primers as claimed in claim 1,
   b) sequencing the amplified products,
   c) blasting the sequence resolved in step (b) against mito database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely family of the animal source of the biological sample,

d) blasting the sequence resolved in step (b) against non-redundant (nr) database of National Centre for Biotechnology Information (NCBI) using BLAST program and determining the most likely genus, species or more precisely the sub-species of the animal source of the biological sample,

e) identifying the most significant alignment of the sequence resolved with cytochrome b gene sequence of the animal identified in steps (c) and (d) respectively and selection of these animals as 'reference animals' for further studies,

f) isolating and amplifying and sequencing the DNA sequences from the reference animal on both strands in triplicate using the primers as claimed in claim 1,

g) aligning the sequences obtained using CLUSTRAL program and identifying the variable sites amongst the animals analyzed,

h) comparing the nucleotide sequences pair-wise to determine the variation among the animals resolved and identifying the nucleotide sequence to which the DNA sequence of the biological sample bears maximum similarity as the source animal of the biological sample.

7. A method as claimed in claim 6 wherein the universal PCR protocol works universally with the DNA template of any unknown animal origin and the universal primers mentioned under column 4.

8. A method as claimed in claim 6 wherein the Amplification reactions should be carried out in 20 μl reaction volume containing approximately 20 ηg of template DNA, 100μm each of dNTPs, 1.25 pmole of each primer, 1.5mM $MgCl_2$, 0.5 unit of Ampli*Taq* Gold (Perkin-Elmer-Cetus, USA) DNA polymerase and 1X PCR buffer (10mM Tris-HCl, pH 8.3, and 50mM KCl). The amplification profiles followed should be: an initial denaturation at 95^0C for 10 min, followed by 35 cycles each of denaturation at 95^0C for 45 s, annealing at 51^0C for 1 min, and extension at 72^0C for 2 min. The extension step at 35^{th} cycles should be held for 10 min.

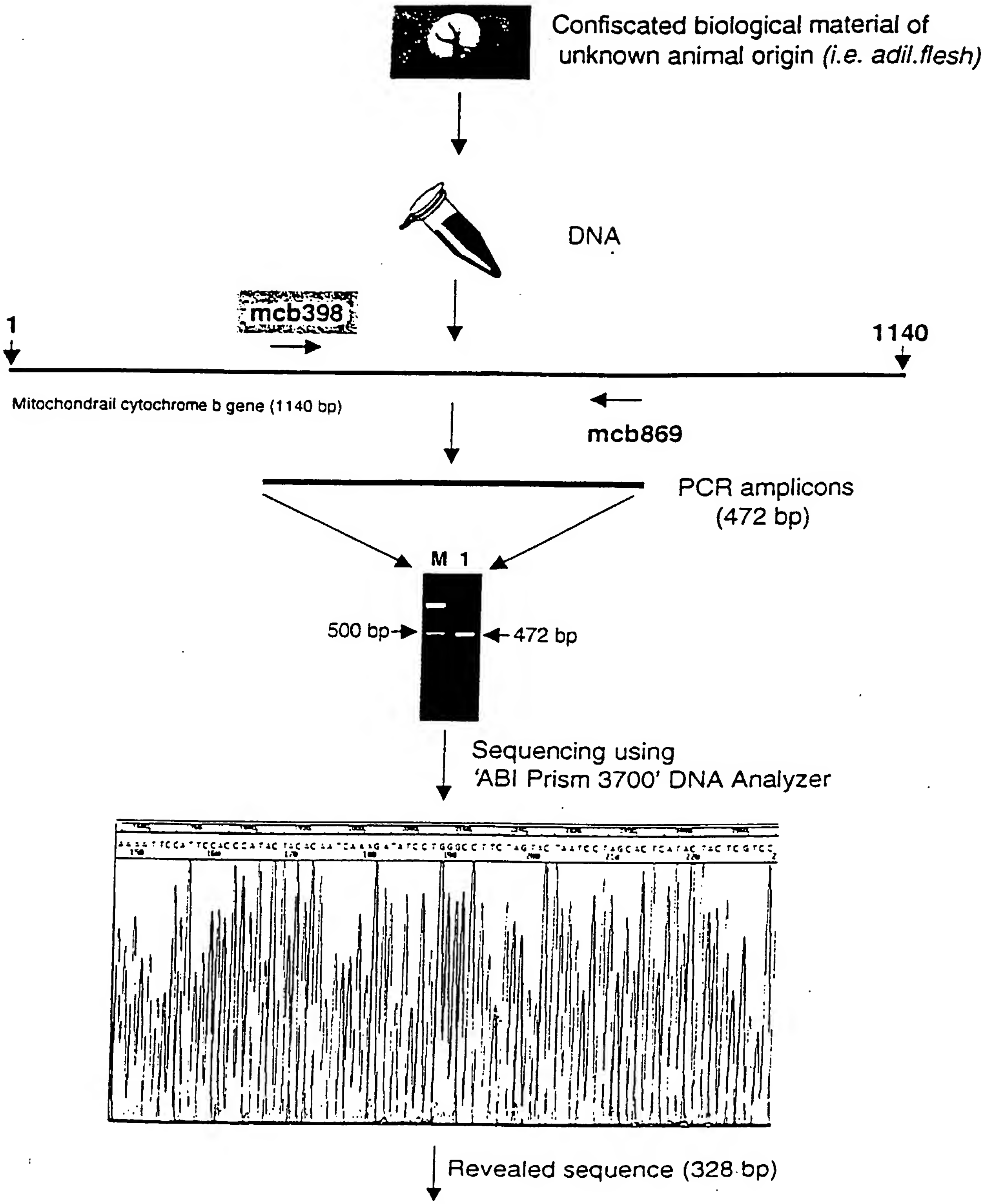
9. A method as claimed in claim 6 wherein the method enables identification of species of analyzed material (i.e. the DNA isolated from confiscated animal remain of unknown origin) using the public databases such as GenBank, NCBI etc.

10. A method as claimed in claim 6 wherein the method is used for animal identification to establish the crime with the criminal beyond a reasonably doubt.

11. A method as claimed in claim 6 wherein the method is used to establish the identity of

biological materials such as skin, horns etc confiscated from animal poachers, if it is that of an endangered species.

12. A method as claimed in claim 6 wherein the method is used for establishment of the identity of confiscated animal parts and products of endangered animal species for the purpose of production of molecular evidence of animal hunting and related crime in the court of law, so that the human violation of the wildlife resources could be controlled.
13. A method as claimed in claim 6 wherein the method is used to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented.
14. A method as claimed in claim 6 wherein the method is used for animal identification to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies.
15. A method as claimed in claim 6 wherein the method is used to provide a universal technique for detection of the origin of blood or blood stains etc collected from the scene of crime related to offences such as murder, rape etc, in order to establish the origin of blood found at scene of crime when it sounds as if criminals have wontedly spread the blood of an animal at the scene of crime, to confuse the crime investigation agencies and forensic scientists with human blood.
16. A method as claimed in claim 6 wherein the method is used so that it can be converted to a (a) COMMERCIAL 'MOLECUALR KIT' and (b) 'DNA CHIPS' based applications for wildlife identification in forensics.



TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACAC
GATTCTTTGCCTTCCACTTCATCCTTCCATTTATCATCTCAGC
TCTAGCAGCAGTCCACCTCCTATTCCTTCACGAGACAGGATCT
AACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCAT
TCCACCCATACTACACAATCAAAGATATCCTGGGCCTTCTAGT
ACTAATCCTAGCACTCATACTACTCGTCCTATTCTCACCAGAC
CTGTTAGGAGACCCCGATAACTACATCCCTGCCAACCCCTCTAA
ATACCCCTCCCCATATCAAGCCTGAAT

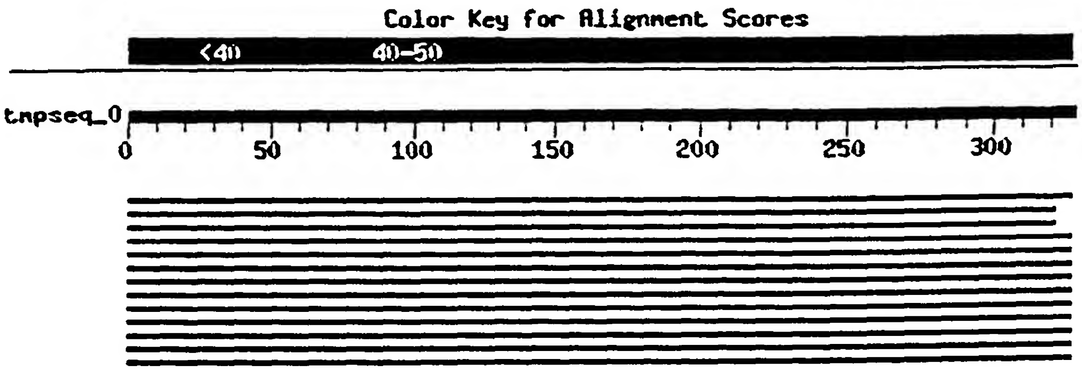
Figure 1 a

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. *'adil.flesh'* using primers **'mcb398'** and **'mcb869'**

Homology search in *'nr'* database using *'BLAST'*

▼

http://www.ncbi.nlm.nih.gov/BLAST/



Sequences producing significant alignments:	Score (bits)	E Value
gb|AY005809.1| ***Panthera pardus*** cytochrome b gene, partial c...	603	e-170
gb|AF053054.1|AF053054 *Panthera tigris sumatrae* isolate Su1...	527	e-147
gb|AF053053.1|AF053053 *Panthera tigris tigris* isolate B7 mi...	527	e-147
gb|AF053050.1|AF053050 *Panthera tigris corbetti* isolate C2 ...	476	e-132
gb|AF053049.1|AF053049 *Panthera tigris corbetti* isolate C1 ...	476	e-132

▼

Selection of reference animals based on above information and further analysis using primers **'mcb398'** and **'mcb869'**

Multiple sequence alignments using *'Autoassembler'*

▼

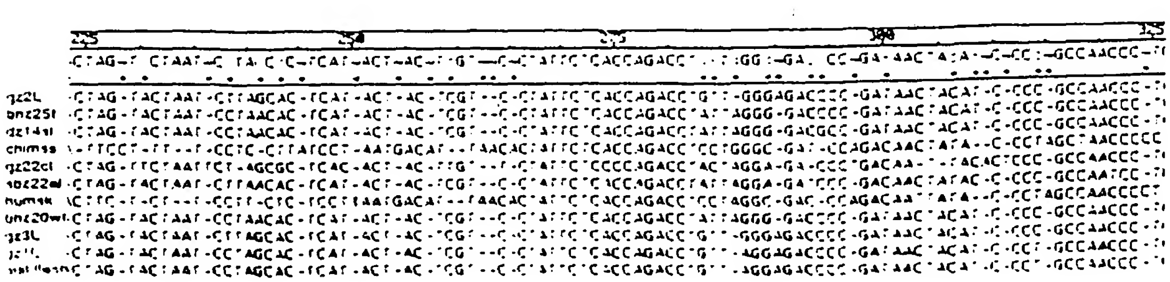


Figure 1 b

NJ-tree showing clustering of *'adil.flesh'* with 'gz1L' i.e.the known normal leopard (*Penthera pardus*)

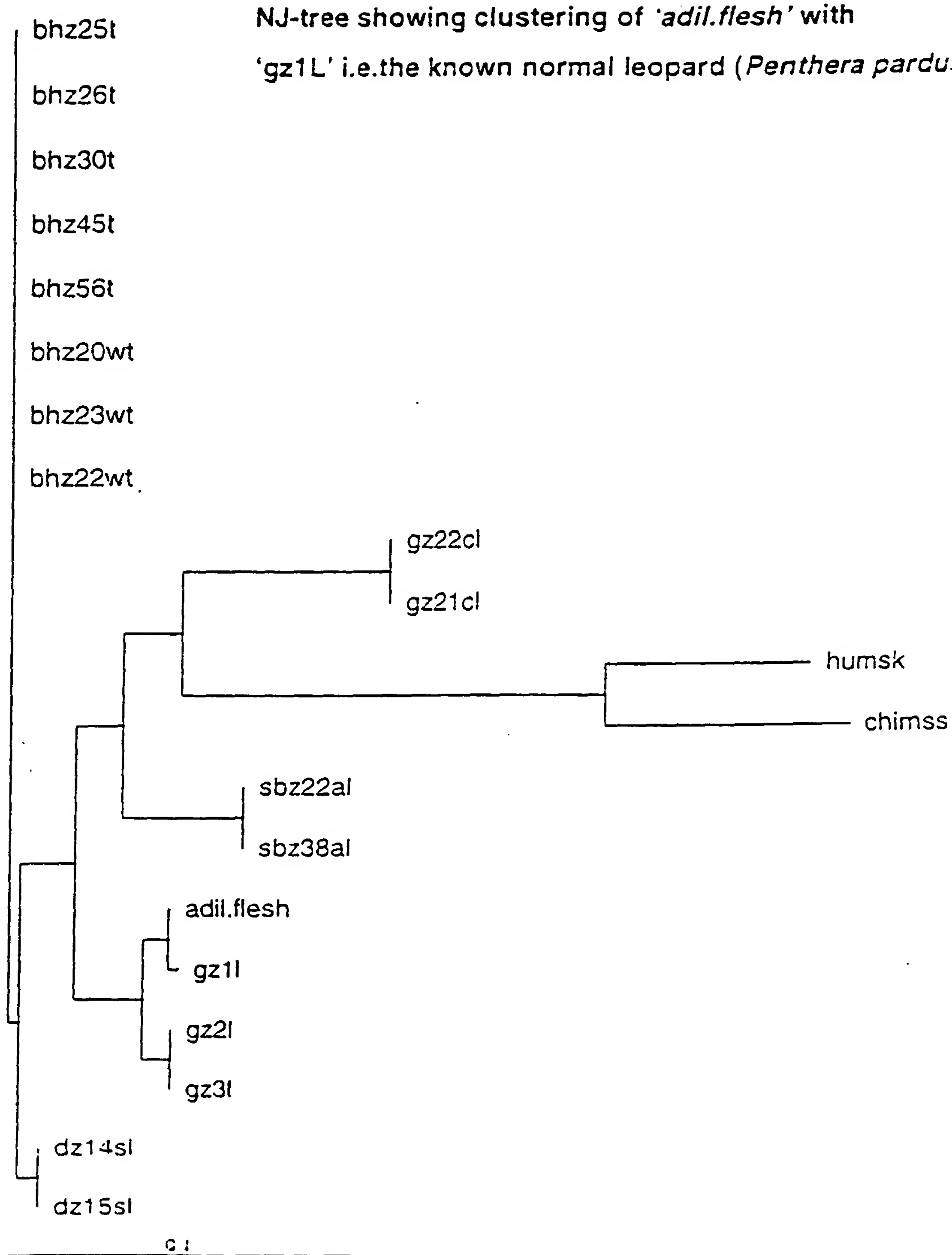


Figure 1c

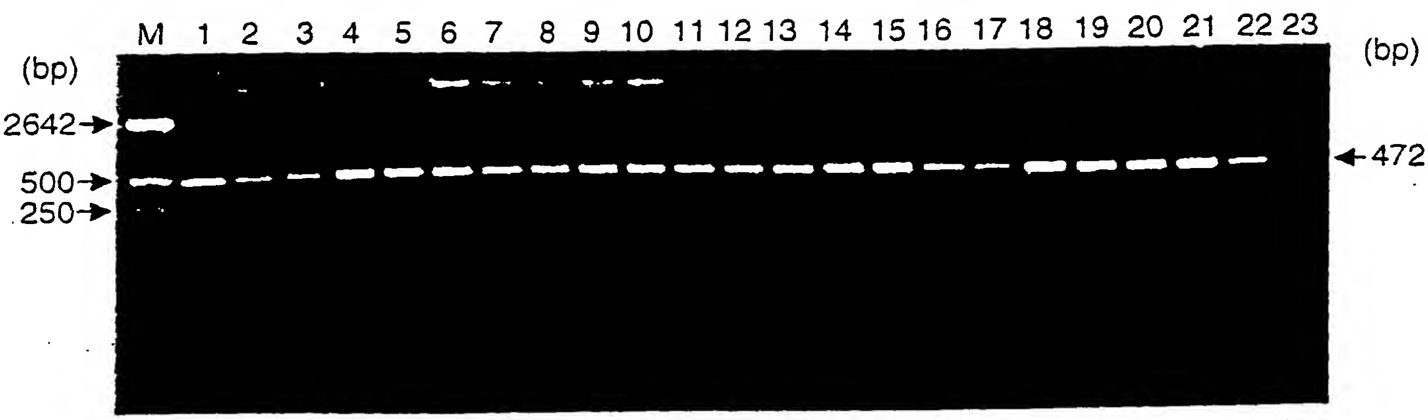

M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23
(bp)
2642
500
250
(bp)
472

Figure 2

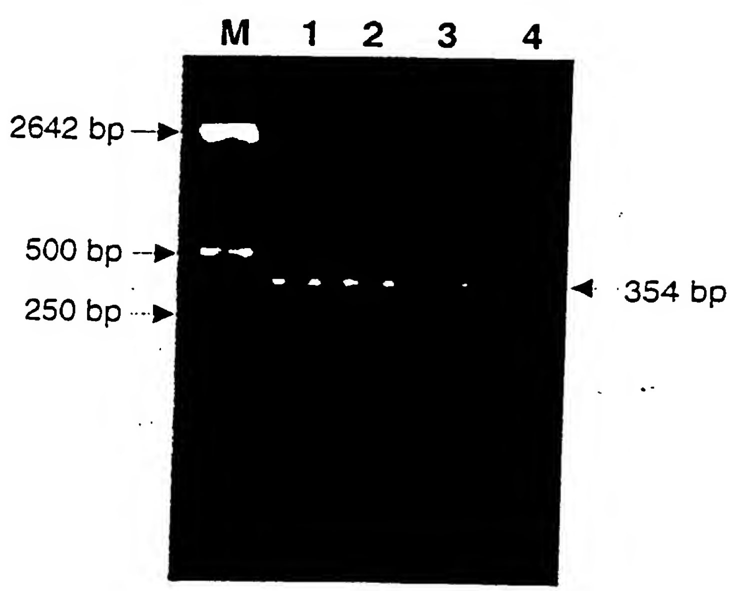


Figure 3

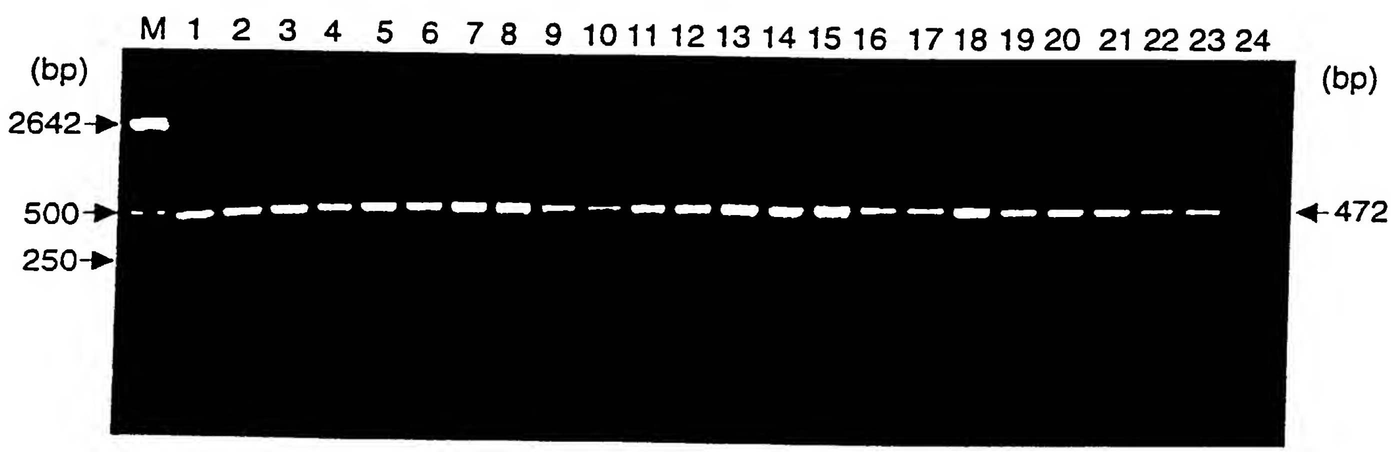

M 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24
(bp)
2642
500
250
(bp)
472

Figure 4

INTERNATIONAL SEARCH REPORT

Inte Application No
PCI/IN 01/00055

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, EPO-Internal, EMBL, WPI Data, PAJ, MEDLINE, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KOCHER T D ET AL: "DYNAMICS OF MITOCHONDRIAL DNA EVOLUTION IN ANIMALS AMPLIFICATION AND SEQUENCING WITH CONSERVED PRIMERS" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES, vol. 86, no. 16, 1989, pages 6196-6200, XP002189444 1989 ISSN: 0027-8424 the whole document ---	1-16
Y	WO 92 05277 A (DAVIDSON WILLIAM SCOTT ;BARTLETT SYLVIA ERNESTINE (CA)) 2 April 1992 (1992-04-02) the whole document ---	1-16

-/--

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
28 February 2002	12/03/2002

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31–70) 340–2040, Tx. 31 651 epo nl, Fax: (+31–70) 340–3016	Hagenmaier, S

Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
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Y	DATABASE EMBL 'Online! ID/AC AAF56513, 28 November 2000 (2000-11-28) ZH NIPPON KAGAKU SENI KENSA KYOKAI: "Animal fibre identification PCR primer #3" XP002191314 abstract ---	1-16
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Y	MATTHEE CONRAD A ET AL: "Cytochrome b phylogeny of the family Bovidae: Resolution within the Alcelaphini, Antilopini, Neotragini, and Tragelaphini." MOLECULAR PHYLOGENETICS AND EVOLUTION, vol. 12, no. 1, June 1999 (1999-06), pages 31-46, XP001053239 ISSN: 1055-7903 the whole document ---	1-16
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A	THOMPSON JULIE D ET AL: "A comprehensive comparison of multiple sequence alignment programs." NUCLEIC ACIDS RESEARCH, vol. 27, no. 13, 1 July 1999 (1999-07-01), pages 2682-2690, XP002191669 ISSN: 0305-1048 the whole document -----	

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ɔrmation on patent family members

Int   ıl Application No
Pᴗ.,ıᴜ 01/00055

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